
MPSRLH
(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:34:45 2000; MasPar time 7.31 Seconds
505.226 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pap
Perfect Score: 1078
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAEGFSDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 189963 segs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseq36
l:geneseq

Statistics: Mean 31.169; Variance 144.272; scale 0.216

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1078	100.0	156	1 R85116	Cell-cycle regulatory	1.18e-85
2	1067	99.0	156	1 W80524	A human multiple tumou	1.20e-84
3	1067	99.0	156	1 W40524	Human MTS1 protein.	1.20e-84
4	1067	99.0	156	1 W74549	Amino acid sequence of	1.20e-84
5	1067	99.0	156	1 W19251	Human multiple tumour	1.20e-84
6	1067	99.0	156	1 W10627	Tumour suppressor p16.	1.20e-84
7	1064	98.7	391	1 W95094	Human p27-p16 fusion p	2.26e-84
8	1064	98.7	391	1 W23534	CDK inhibitory fusion	2.26e-84
9	1057	98.1	237	1 W95105	Truncated p27/p16 fusi	9.86e-84
10	1057	98.1	252	1 W35106	Truncated p27/p16 fusi	9.86e-84
11	1057	98.1	334	1 W35103	CDK inhibitory fusion	9.86e-84
12	1057	98.1	365	1 W23536	CDK inhibitory fusion	9.86e-84
13	1057	98.1	365	1 W95096	Human p16p27 fusion pr	9.86e-84
14	1057	98.1	365	1 W95107	Human p16p27 fusion pr	9.86e-84
15	1057	98.1	380	1 W35095	Human p16(GS)p27 fusi	9.86e-84
16	1057	98.1	380	1 W23535	CDK inhibitory fusion	9.86e-84
17	1056	98.0	156	1 W19252	Human multiple tumour	1.22e-83
18	1050	97.4	156	1 W19253	Human multiple tumour	4.31e-83
19	1037	96.2	348	1 W95104	Truncated p27/p16 fusi	6.65e-82
20	1030	95.5	148	1 R81701	Multiple tumour suppre	2.90e-81
21	1030	95.5	148	1 R80940	Human multiple tumour	2.90e-81
22	1030	95.5	151	1 R33401	Inhibitor of cyclin de	2.90e-81
23	921	85.4	157	1 R85114	Cell-cycle regulatory	2.59e-71

24	737	68.4	130	1 R85118	Cell-cycle regulatory	1.33e-54
25	735	68.2	105	1 W74550	Amino acid sequence 1	2.02e-54
26	735	68.2	105	1 R80947	Human multiple tumour	2.02e-54
27	735	68.2	105	1 W19254	Human MTS1-beta prot	2.02e-54
28	735	68.2	105	1 W40525	Human MTS1E1-beta prot	2.02e-54
29	735	68.2	105	1 R81700	Multiple tumour suppre	2.02e-54
30	735	68.2	105	1 W80525	A human multiple tumou	2.02e-54
31	729	67.6	130	1 W70823	Mouse multiple tumour	7.06e-54
32	725	67.3	138	1 R80948	Human multiple tumour	1.62e-53
33	725	67.3	138	1 W80526	A human multiple tumou	1.62e-53
34	725	67.3	138	1 R81702	Multiple tumour suppre	1.62e-53
35	725	67.3	138	1 W74553	Amino acid sequence 2	1.62e-53
36	725	67.3	138	1 W40526	Human MTS2 protein.	1.62e-53
37	725	67.3	138	1 W19255	Human multiple tumour	1.62e-53
38	713	66.1	138	1 R85117	Cell-cycle regulatory	1.97e-52
39	676	62.7	168	1 W80527	Mouse multiple tumour	4.31e-49
40	556	51.6	138	1 R85115	Cell-cycle regulatory	2.58e-38
41	484	44.9	67	1 W16324	Human INK4a-p16 C-term	6.67e-32
42	473	43.9	125	1 W16322	Murine INK4a-p16 C-ter	6.31e-31
43	473	43.9	125	1 R85120	Cell-cycle regulatory	6.31e-31
44	446	41.4	85	1 R85113	Cell-cycle regulatory	1.54e-28
45	446	41.4	127	1 R85119	Cell-cycle regulatory	1.54e-28

ALIGNMENTS

RESULT 1
ID R85116 standard; Protein; 156 AA.
AC R85116;
DT 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein p16.
KW Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
KW CCR; cancer; cell proliferation.
OS Homo sapiens.
PN WO9528483-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U046336.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
DR MPI; 95-373798/48.
DR N-PSDB; T02962.

PT New cell cycle regulating proteins bind to cyclin dependent kinase -
and related nucleic acids, antibodies etc., used in diagnosis and
therapy of abnormal cell proliferation, degeneration etc.
PS Claim 1; Page 76-77; 109pp; English.
CC The human cell-cycle regulatory (CCR) protein p16 (R85116) was
obt'd. by expression of a cDNA clone (T02962) isolated in a 2-hybrid
screening assay. CCR p16 specifically inhibits the activity of
CC cyclin-dependent kinases during various stages of the cell cycle,
CC and can be used in the treatment and diagnosis of proliferative
CC disorders. 156 AA;
SQ Sequence 156 AA;

Query Match 100.0%; Score 1078; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.18e-85;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	MDPAGSSMEPSADWLATAAARGVEVRALLEVALPAPNSYGRPIQVMGMSARVA	60
QY	1	MDPAGSSMEPSADWLATAAARGVEVRALLEVALPAPNSYGRPIQVMGMSARVA	60
Db	61	ELLLLHGAEPNCADPATLTPVHDAREGFLDTLVLRHAGARLDVDRGRLPVDLAE	120
QY	61	ELLLLHGAEPNCADPATLTPVHDAREGFLDTLVLRHAGARLDVDRGRLPVDLAE	120
Db	121	LGHDRVARYLRAAAGGTGSGNHARIDAEGFSDIPD	156
QY	121	LGHDRVARYLRAAAGGTGSGNHARIDAEGFSDIPD	156

RESULT 2
 ID W80524 standard; Protein; 156 AA.
 AC W80524;
 DT 03-FEB-1999 (first entry)
 DE A human multiple tumour suppressor 1 (MTS1) protein.
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
 OS Homo sapiens.
 PN US5843756-A.
 PD 01-DEC-1998.
 PE 28-JUL-1995; 058735.
 PR 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI: 99-044585/04.
 DR N-PSDB: V70583.
 PT Mouse multiple tumour suppressor gene segment - useful for primer design
 PS Disclosure: Columns 65-66; 80pp; English.
 CC The present sequence represents a human multiple tumour suppressor 1 (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
 CC Sequence 156 AA;
 SQ

Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 Db 121 LGRDVARYLRAAAGTGRGSHARIDAAEGSPDIPD 156
 QY 121 LGRDVARYLRAAAGTGRGSHARIDAAEGSPDIPD 156
 RESULT 4
 ID W74549 standard; Protein; 156 AA.
 AC W74549;
 DT 04-DEC-1998 (first entry)
 DE Amino acid sequence of multiple tumour suppressor 1.
 KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
 KW Somatic mutation; gene therapy.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PE 07-JUN-1995; 480810.
 PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 14-APR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI: 98-494842/42.
 DR N-PSDB: V53819.
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences - useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS mutation(s)
 PS Disclosure; Column 63-64; 73pp; English.
 CC This is the amino acid sequence of the multiple tumour suppressor 1 (MTS-1) protein, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can also be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
 CC Sequence 156 AA;
 SQ

Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 Db 121 LGRDVARYLRAAAGTGRGSHARIDAAEGSPDIPD 156
 QY 121 LGRDVARYLRAAAGTGRGSHARIDAAEGSPDIPD 156
 RESULT 3
 ID W40524 standard; Protein; 156 AA.
 AC W40524;
 DT 15-JUL-1998 (first entry)
 DE Human MTS1 protein.
 KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition.
 OS Homo sapiens.
 PN US5739027-A.
 PD 14-APR-1998.
 PE 07-JUN-1995; 487033.
 PR 07-JUN-1995; US-487033.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI: 98-250421/22.
 DR N-PSDB: V11238.
 PT DNA specific for Multiple Tumour Suppressor 1el-beta gene - are useful for the diagnosis of cancers related to MTS1el-beta mutation(s) and their treatment
 PS Disclosure; Column 63-64; 72pp; English.
 CC This sequence represents a human multiple tumour suppression protein,

CC MTS1. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
 CC Sequence 156 AA;
 SQ

Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAE 120
 Db 121 LGRDVARYLRAAAGTGRGSHARIDAAEGSPDIPD 156
 QY 121 LGRDVARYLRAAAGTGRGSHARIDAAEGSPDIPD 156

RESULT 4
 ID W74549 standard; Protein; 156 AA.
 AC W74549;
 DT 04-DEC-1998 (first entry)
 DE Amino acid sequence of multiple tumour suppressor 1.
 KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
 KW Somatic mutation; gene therapy.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PE 07-JUN-1995; 480810.
 PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 14-APR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI: 98-494842/42.
 DR N-PSDB: V53819.
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences - useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS mutation(s)
 PS Disclosure; Column 63-64; 73pp; English.
 CC This is the amino acid sequence of the multiple tumour suppressor 1 (MTS-1) protein, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can also be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
 CC Sequence 156 AA;
 SQ

Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 1.20e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRPRPQVMMGSAVA 60

Db 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

Db 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

QY 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

RESULT 5

ID W19251 standard; Protein; 156 AA.

AC W19251;

DT 10-SEP-1997 (first entry)

DE Human multiple tumour suppressor 1 gene product.

KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.

OS Homo sapiens.

PN US5624819-A.

PD 29-APR-1997.

PF 18-MAR-1994; 214582.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 14-APR-1994; US-215087.

PR 01-JUN-1994; US-227369.

PR 17-MAR-1995; WO-003537.

PR 07-JUN-1995; US-474177.

PA (MYRI-) MYRIAD GENETICS INC.

PA (UTAH) UNIV UTAH RES FOUND.

PI Cannon-Albright LA, Kamb A, Skolnick MH;

DR WPI: 97-258217/23.

DR N-PSDB; T72311.

PT Human mutant multiple tumour suppressor gene sequences - for

PS production of recombinant mutant polypeptide(s)

PS Claim 1; Columns 61-64; 72pp; English.

CC The present sequence the human multiple tumour suppressor 1

CC (MTS1) gene product, useful in cancer diagnosis.

SQ Sequence 156 AA;

Query Match

Best Local Similarity 99.0%; Score 1067; DB 1; Length 156;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MEPAAGSMPEPSADWLATAAARGVEEVREALLBAGALPNAPNSYGRRPQVMMGMSARVA 60

QY 1 MDPAAGSMPEPSADWLATAAARGVEEVREALLBAGALPNAPNSYGRRPQVMMGMSARVA 60

Db 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

QY 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

Db 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

QY 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

RESULT 6

ID W10627 standard; Protein; 156 AA.

AC W10627;

DT 28-OCT-1997 (first entry)

DE Tumour suppressor p16.

KW Tumour suppressor p16; inhibitor; cyclin-dependent kinase 4; CDK4;

KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;

KW anti-angiogenic activity; hyperproliferative disorder.

OS Homo sapiens.

PN WO9703635-A2.

PD 06-FEB-1997.

PF 17-JUL-1996; U11787.

PR 17-JUL-1995; US-502881.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Jin X, Roth J;

DR WPI: 97-132336/12.

DR N-PSDB; T60951.

PT Expression construct contg. DNA for tumour suppressor p16 - to
 PT restore p16 activity to transformed cells, useful for treating lung
 PT or bladder cancer or melanoma
 PS Disclosure; Fig 1b; 92pp; English.
 CC This sequence represents the tumour suppressor p16. The DNA encoding
 CC this sequence is joined to a promoter functional in eukaryotic cells and
 CC used in the expression construct of the invention. p16 is an inhibitory
 CC subunit, which is involved in the control of cyclin-dependent kinase 4
 CC activity, and functions as a tumour suppressor. By detecting this
 CC sequence or the DNA encoding it, cancer cells can be detected. When the
 CC nucleic acid molecule is in the sense orientation, the expression
 CC construct can be used to restore p16 function in a cell, particularly by
 CC reversing the transformed phenotype in tumours, especially lung or
 CC bladder cancer or melanoma. It may also have anti-angiogenic activity,
 CC and inhibit hyperproliferative disorders, e.g. restenosis. When the
 CC nucleic acid molecule is inserted in the antisense orientation, the
 CC expression construct inhibits p16 function. Reduced or increased levels
 CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by
 CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
 CC or immunoassay.
 SQ Sequence 156 AA;

Query Match 99.0%; Score 1067; DB 1; Length 156;

Best Local Similarity 98.7%; Pred. No. 1.20e-84;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MEPAAGSMPEPSADWLATAAARGVEEVREALLBAGALPNAPNSYGRRPQVMMGMSARVA 60

QY 1 MDPAAGSMPEPSADWLATAAARGVEEVREALLBAGALPNAPNSYGRRPQVMMGMSARVA 60

Db 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

QY 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAE 120

Db 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

QY 121 LGHRDVARYLRAAAGTGRGSHNARIDAAEGPSDIPD 156

RESULT 7

ID W95094 standard; Protein; 391 AA.

AC W95094;

DT 25-MAY-1999 (first entry)

DE Human p27-p16 fusion protein.

KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;

KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;

KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;

KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;

KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;

KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;

KW tachycardia; human; p27; p16.

OS Homo sapiens.

PN WO9906540-A2.

PD 11-FEB-1999.

PF 29-JUL-1998; U15759.

PR 29-JUL-1997; US-902572.

PA (MITO-) MITOTIX INC.

PI Beach DH, Gyuris J, Lamphere L;

DR WPI: 99-153770/13.

DR N-PSDB; X26220.

PT Fusion and chimaeric proteins including cyclin-dependent kinase

PT binding motif - used for regulation of cell proliferation and

PT differentiation, for treatment of, e.g. vascular injury, cancers,

PT fibrosis and neurodegeneration

PS Claim 63; Page 70-72; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases

CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant

CC transfection system (A) that comprises: (i) first gene construct

CC comprising a sequence encoding an inhibitory polypeptide containing at

CC least one CDK-binding motif for binding and inhibiting activity of a CDK,

CC linked to a transcription regulator functional in eukaryotic cells; (ii)

CC second gene construct comprising a sequence encoding a polypeptide that

CC promotes endothelialisation, and (iii) a gene delivery composition for

CC delivering the GCs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
 CC consists of at least one CDK-binding motif and a TCP. (A) are used to
 CC treat vascular wounds that involve a break in the endothelium and
 CC excessive proliferation of smooth muscle, particularly restenosis but
 CC more generally any repair of cardiovascular damage, arteriosclerotic
 CC lesions or for endothelialisation of synthetic vascular grafts. More
 CC generally, FP are used to treat unwanted cellular proliferation in a very
 CC wide range of situations, e.g. for treating vascular diseases as above;
 CC fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many
 CC tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration;
 CC acne; also to control hair growth (e.g. to prevent hair loss caused by
 CC chemotherapy or radiation); periodontal disease; to treat tachycardia;
 CC to inhibit spermatogenesis etc. Chimaeric proteins comprising CDK-binding
 CC motifs from two or more different proteins bind to CDKs so inhibit cell
 CC cycle progression, particularly smooth muscle cell proliferation. The
 CC gene constructs may also be used to produce FP in cell cultures, for
 CC production or for regulating cell differentiation in vitro. The present
 CC sequence represents a human p27-p16 fusion protein.
 SQ Sequence 391 AA;

Query Match 98.7%; Score 1064; DB 1; Length 391;
 Best Local Similarity 98.7%; Pred. No. 2.26e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 236 MORAAGSMPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSRVA 295
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSRVA 60
 Db 296 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVHLRAGARLDVRDANGRLPVDLAE 355
 QY 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVHLRAGARLDVRDANGRLPVDLAE 120
 Db 356 LGRDVARYLRAAGGTRGSHARIDAAGPSDIPD 391
 QY 121 LGRDVARYLRAAGGTRGSHARIDAAGPSDIPD 156

RESULT 8

ID W3534 standard; Protein; 391 AA.
 AC W3534;
 DE Truncated p27/p16 fusion protein.
 DE 16-MAR-1998 (first entry)
 KW CDK inhibitory fusion protein #1.
 KW Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
 KW chimeric polypeptide; human; binding motif; proliferation control;
 KW cell differentiation; cell-cycle inhibitor; proliferative disorder;
 KW tissue degeneration; therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 1..7
 FT Misc_difference 205..219 /note= "poly-His tag"
 FT Misc_difference 205..219 /note= "(Gly/Ser)2 linker"
 FT W09727297-A1.
 FN 31-JUL-1997.
 PD 17-JAN-1997; U00569.
 PR 23-JAN-1996; US-589981.
 PA (MITO-) MITOTIX INC.
 PI Beach D, Gyuris J, Lamphere L;
 DR WPI; 97-393685/36.
 DR N-PSDB; T74051.
 PT Chimeric inhibitor of cyclin dependent kinase - useful for gene
 PT therapy of cancer and other proliferative and differentiative
 PT diseases
 PS Claim 40; Page 38-40; 58pp; English.
 CC This sequence represents a chimeric polypeptide of the invention. It was
 CC derived from a fusion of the human p27 and p16 cDNA sequences. The
 CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
 CC binding motifs from at least two different proteins that bind to CDKs.
 CC The protein controls proliferation and/or differentiation of cells,

CC particularly they inhibit cell-cycle progression. They can be used to
 CC treat a wide range of proliferative disorders, e.g. cancer, leukaemia,
 CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They
 CC can also treat diseases associated with de-differentiation or
 CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
 CC diseases, gastric ulcers and autonomous diseases of the peripheral
 CC nervous system. Other applications include reducing growth of hair and
 CC protecting hair follicle cells against cytotoxic treatments, cosmetically
 CC to treat various forms of folliculitis, and to inhibit spermatogenesis or
 CC oogenesis. The chimeric proteins can also be used in vitro to maintain
 CC cells, especially neurons intended for testing specific activity of
 CC trophic factors, at selected points in the cell cycle. The proteins are
 CC more active inhibitors of the CDK/cyclin complex than binding motifs used
 CC individually (since they may bind to CDK involved in different stages of
 CC the cell cycle).
 SQ Sequence 391 AA;

Query Match 98.7%; Score 1064; DB 1; Length 391;
 Best Local Similarity 98.7%; Pred. No. 2.26e-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 236 MORAAGSMPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSRVA 295
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSRVA 60
 Db 296 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVHLRAGARLDVRDANGRLPVDLAE 355
 QY 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVHLRAGARLDVRDANGRLPVDLAE 120
 Db 356 LGRDVARYLRAAGGTRGSHARIDAAGPSDIPD 391
 QY 121 LGRDVARYLRAAGGTRGSHARIDAAGPSDIPD 156

RESULT 9

ID W95105 standard; Protein; 237 AA.
 AC W95105;
 DE Truncated p27/p16 fusion protein.
 DE 25-MAY-1999 (first entry)
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KW tachycardia; human; p27; p16; truncated.
 OS Homo sapiens.
 PN W0906540-A2.
 PD 11-FEB-1999.
 PF 29-JUL-1998; U15759.
 PR 29-JUL-1997; US-902572.
 PA (MITO-) MITOTIX INC.
 PI Beach D, Gyuris J, Lamphere L;
 DR WPI; 99-153770/13.
 DR N-PSDB; X26233.
 PT Fusion and chimaeric proteins including cyclin-dependent kinase
 PT binding motif - used for regulation of cell proliferation and
 PT differentiation, for treatment of, e.g. vascular injury, cancers,
 PT fibrosis and neurodegeneration
 PS Claim 63; Page 85; 88pp; English.
 CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)
 CC second gene construct comprising a sequence encoding a polypeptide that
 CC promotes endothelialisation, and (iii) a gene delivery composition for
 CC delivering the GCs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP

CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a human truncated p27/p16 fusion protein.
SQ Sequence 237 AA;

Query Match 98.1%; Score 1057; DB 1; Length 237;
Best Local Similarity 99.4%; Pred. No. 9.86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 83 DPAAGSSMEPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSRVAE 142
QY 2 DPAAGSSMEPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSRVAE 61

Db 143 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDANGRLPVDLAEEL 202
QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDANGRLPVDLAEEL 121

Db 203 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 237
QY 122 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 10
ID W95106 standard; Protein; 252 AA.
AC W95106;
DE 25-MAY-1999 (first entry)
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16; truncated.
OS Homo sapiens.
PN W09906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; OS-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI: 99-153770/13.
DR N-PSDB: X26234.
PT Fusion and chimeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 63; Page 85; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a human truncated p27/p16 fusion protein.
SQ Sequence 252 AA;

Query Match 98.1%; Score 1057; DB 1; Length 252;
Best Local Similarity 99.4%; Pred. No. 9.86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 98 DPAAGSSMEPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSRVAE 157
QY 2 DPAAGSSMEPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSRVAE 61

Db 158 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDANGRLPVDLAEEL 217
QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDANGRLPVDLAEEL 121

Db 218 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 252
QY 122 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 11
ID W95103 standard; Protein; 334 AA.
AC W95103;
DE 25-MAY-1999 (first entry)
KW Truncated p27/p16 fusion protein.
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16; truncated.
OS Homo sapiens.
PN W09906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; OS-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI: 99-153770/13.
DR N-PSDB: X26234.
PT Fusion and chimeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 63; Page 83; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a human truncated p27/p16 fusion protein.
SQ Sequence 334 AA;

Query Match 98.1%; Score 1057; DB 1; Length 334;
Best Local Similarity 99.4%; Pred. No. 9.86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 180 DPAAGSSMEPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSRVAE 239
QY 2 DPAAGSSMEPSADMLATAAARGVEEVALLAEAGALPNAPNSYGRRPQVMMGSRVAE 61

Db 240 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDANGRLPVDLAEEL 299
QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVHLRAGARLDVDRDANGRLPVDLAEEL 121

Db 300 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 334
QY 122 GHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 12
ID W23536 standard; Protein; 365 AA.

AC W23536;
DT 16-MAR-1998 (first entry)
DE CDK inhibitory fusion protein p16p27.
KW Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
KW chimeric polypeptide; human; binding motif; proliferation control;
KW cell differentiation; cell-cycle inhibitor; proliferative disorder;
KW tissue degeneration; therapy.
OS Homo sapiens.
PN WO9727297-A1.
PD 31-JUL-1997.
PF 17-JAN-1997: U00569.
PR 23-JAN-1996: US-589981.
PA (MITO-) MITOTIX INC.
PI Beach D, Gyuris J, Lamphere L;
DR N-PSDB; T74053.
PT Chimeric inhibitor of cyclin dependent kinase - useful for gene
therapy of cancer and other proliferative and differentiative
PT diseases
PS Claim 40; Page 46-48; 58pp; English.
CC This sequence represents a chimeric polypeptide of the invention. It was
derived from a fusion of the human p27 and p16 cDNA sequences. The
chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
binding motifs from at least two different proteins that bind to CDKs.
CC The protein controls proliferation and/or differentiation of cells.
CC particularly they inhibit cell-cycle progression. They can be used to
treat a wide range of proliferative disorders, e.g. cancer, leukaemia,
CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They
can also treat diseases associated with de-differentiation or
CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
diseases, gastric ulcers and autonomous diseases of the peripheral
CC nervous system. Other applications include reducing growth of hair and
protecting hair follicle cells against cytotoxic treatments, cosmetically
CC to treat various forms of folliculitis, and to inhibit spermatogenesis or
oogenesis. The chimeric proteins can also be used in vitro to maintain
CC cells, especially neurons intended for testing specific activity of
trophic factors, at selected points in the cell cycle. The proteins are
CC more active inhibitors of the CDK/cyclin complex than binding motifs used
individually (since they may bind to CDK involved in different stages of
CC the cell cycle).
SQ Sequence 365 AA;

Query Match 98.1%; Score 1057; DB 1; Length 365;
Best Local Similarity 99.4%; Pred. No. 9,86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 12 DPAAGSMPEPSADWLATAAARGVEEVRALEAGALPNAPNSYGRPIQVMMGSAARVAE 71
QY 2 DPAAGSMPEPSADWLATAAARGVEEVRALEAGALPNAPNSYGRPIQVMMGSAARVAE 61
Db 72 LLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAEL 131
QY 62 LLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAEL 121
Db 132 GHRDVARYLRAAGGTRGNSHARIDAEGPSDIPD 166
QY 122 GHRDVARYLRAAGGTRGNSHARIDAEGPSDIPD 156

RESULT 13
ID W95096 standard; Protein; 365 AA.
AC W95096;
DT 25-MAY-1999 (first entry)

DE Human p16p27 fusion protein.
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
OS Homo sapiens.
PN WO9506540-A2.

PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; US-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI; 99-153770/13.
DR N-PSDB; X26224.
PT Fusion and chimeric proteins including cyclin-dependent kinase
binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 63; Page 78-79; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
(CDKs), particularly CDK/cyclin complexes. It provides a recombinant
transfection system (A) that comprises: (i) first gene construct
comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a human p16p27 fusion protein.
SQ Sequence 365 AA;

Query Match 98.1%; Score 1057; DB 1; Length 365;
Best Local Similarity 99.4%; Pred. No. 9,86e-84;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 12 DPAAGSMPEPSADWLATAAARGVEEVRALEAGALPNAPNSYGRPIQVMMGSAARVAE 71
QY 2 DPAAGSMPEPSADWLATAAARGVEEVRALEAGALPNAPNSYGRPIQVMMGSAARVAE 61
Db 72 LLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAEL 131
QY 62 LLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAEL 121
Db 132 GHRDVARYLRAAGGTRGNSHARIDAEGPSDIPD 166
QY 122 GHRDVARYLRAAGGTRGNSHARIDAEGPSDIPD 156

RESULT 14
ID W95107 standard; Protein; 365 AA.
AC W95107;

DT 25-MAY-1999 (first entry)
DE Human p16p27 fusion protein.
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
OS Homo sapiens.
PN WO9506540-A2.

PD 11-FEB-1999.
PF 29-JUL-1998; U15759.

PR 29-JUL-1997; US-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI; 99-153770/13.
DR N-PSDB; X26235.
PT Fusion and chimeric proteins including cyclin-dependent kinase
binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 63; Page 86; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)
 CC second gene construct comprising a sequence encoding a polypeptide that
 CC promotes endothelialisation, and (iii) a gene delivery composition for
 CC delivering the GCs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
 CC consists of at least one CDK-binding motif and a TCP. See X26220 for
 CC detailed uses of the recombinant transfection system. The present
 CC sequence represents a human p16p27 fusion protein.
 SQ Sequence 365 AA;

Query Match 98.1%; Score 1057; DB 1; Length 365;
 Best Local Similarity 99.4%; Pred. No. 9.86e-84;
 Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 211 DPAAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSYGRRPDIQYMMGMSARVAE 270
 QY 2 DPAAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSYGRRPDIQYMMGMSARVAE 61
 Db 271 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAEEL 330
 QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAEEL 121
 Db 331 GHRDVARYLRAAAGGTRGSHNARIDAAEGPSDIPD 365
 QY 122 GHRDVARYLRAAAGGTRGSHNARIDAAEGPSDIPD 156

RESULT 15
 ID W95095 standard; Protein; 380 AA.
 AC W95095;
 DT 25-MAY-1999 (first entry)
 DE Human p16(GS)p27 fusion protein.
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KW tachycardia; human; p27; p16.
 OS Homo sapiens.
 PN WO9906540-A2.
 PD 11-FEB-1999.
 PF 29-JUL-1998; U15759.
 PR 29-JUL-1997; US-902572.
 PA (MITO-) MITOTIX INC.
 PI Beach DH, Gyuris J, Lamphere L;
 DR WPI: 99-153770/13.
 DR N-PSDB; X26223.
 PT Fusion and chimeric proteins including cyclin-dependent kinase
 PT binding motif - used for regulation of cell proliferation and
 PT differentiation, for treatment of, e.g. vascular injury, cancers,
 PT fibrosis and neurodegeneration
 PS Claim 63; Page 74-76; 88pp; English.
 CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)
 CC second gene construct comprising a sequence encoding a polypeptide that
 CC promotes endothelialisation, and (iii) a gene delivery composition for
 CC delivering the GCs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular

CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
 CC consists of at least one CDK-binding motif and a TCP. See X26220 for
 CC detailed uses of the recombinant transfection system. The present
 CC sequence represents a human p16(GS)p27 fusion protein.
 SQ Sequence 380 AA;

Query Match 98.1%; Score 1057; DB 1; Length 380;
 Best Local Similarity 99.4%; Pred. No. 9.86e-84;
 Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 12 DPAAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSYGRRPDIQYMMGMSARVAE 71
 QY 2 DPAAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSYGRRPDIQYMMGMSARVAE 61
 Db 72 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAEEL 131
 QY 62 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRDAGRLPVDLAEEL 121
 Db 132 GHRDVARYLRAAAGGTRGSHNARIDAAEGPSDIPD 166
 QY 122 GHRDVARYLRAAAGGTRGSHNARIDAAEGPSDIPD 156

Search completed: Thu Jul 20 08:34:54 2000
 Job time : 9 secs.

W P S R L H (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:36:50 2000; MasPar time 5.60 Seconds
401.877 Million cell updates/sec
Tabular output not generated.

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pep
Perfect Score: 1078
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAEAGSPDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 29.074; Variance 136.818; scale 0.212

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description	Pred. No.
1	1078	100.0	156	4 PCT-US95-0 Sequence 2, Applicatio	4.93e-85
2	1078	100.0	156	3 US-08-581- Sequence 2, Applicatio	4.93e-85
3	1078	100.0	156	2 US-08-306- Sequence 2, Applicatio	4.93e-85
4	1078	100.0	156	2 US-08-893- Sequence 2, Applicatio	4.93e-85
5	1078	100.0	156	2 US-08-627- Sequence 2, Applicatio	4.93e-85
6	1067	99.0	156	1 US-08-480- Sequence 2, Applicatio	4.84e-84
7	1067	99.0	156	2 US-08-486- Sequence 2, Applicatio	4.84e-84
8	1067	99.0	156	2 US-08-848- Sequence 2, Applicatio	4.84e-84
9	1067	99.0	156	1 US-08-487- Sequence 2, Applicatio	4.84e-84
10	1067	99.0	156	2 US-08-508- Sequence 2, Applicatio	4.84e-84
11	1067	99.0	156	3 US-09-120- Sequence 2, Applicatio	4.84e-84
12	1067	99.0	156	1 US-08-474- Sequence 2, Applicatio	4.84e-84
13	1067	99.0	157	4 PCT-US96-0 Sequence 5, Applicatio	4.84e-84
14	1064	98.7	391	1 US-08-589- Sequence 2, Applicatio	9.03e-84
15	1030	95.5	148	4 PCT-US93-0 Sequence 4, Applicatio	1.05e-80
16	1030	95.5	148	3 US-08-384- Sequence 2, Applicati	1.05e-80
17	1030	95.5	148	3 US-08-384- Sequence 2, Applicati	1.05e-80
18	1030	95.5	148	1 US-08-154- Sequence 4, Applicati	1.05e-80
19	921	85.4	157	3 US-08-581- Sequence 12, Applicati	6.75e-71
20	737	68.4	130	4 PCT-US95-0 Sequence 8, Applicatio	2.05e-54
21	737	68.4	130	2 US-08-627- Sequence 8, Applicatio	2.05e-54
22	737	68.4	130	3 US-08-581- Sequence 8, Applicatio	2.05e-54
23	735	68.2	105	3 US-09-120- Sequence 14, Applicati	3.09e-54

24	735	68.2	105	1 US-08-480- Sequence 14, Applicati	3.09e-54
25	735	68.2	105	1 US-08-474- Sequence 14, Applicati	3.09e-54
26	735	68.2	105	1 US-08-487- Sequence 14, Applicati	3.09e-54
27	735	68.2	105	2 US-08-848- Sequence 14, Applicati	3.09e-54
28	735	68.2	105	2 US-08-486- Sequence 14, Applicati	3.09e-54
29	735	68.2	105	2 US-08-508- Sequence 14, Applicati	3.09e-54
30	729	67.6	130	2 US-08-508- Sequence 4, Applicatio	1.06e-53
31	725	67.3	138	4 PCT-US95-0 Sequence 4, Applicatio	2.42e-53
32	725	67.3	138	3 US-08-384- Sequence 25, Applicati	2.42e-53
33	725	67.3	138	2 US-08-627- Sequence 4, Applicatio	2.42e-53
34	725	67.3	138	1 US-08-474- Sequence 16, Applicati	2.42e-53
35	725	67.3	138	1 US-08-487- Sequence 16, Applicati	2.42e-53
36	725	67.3	138	1 US-08-480- Sequence 16, Applicati	2.42e-53
37	725	67.3	138	2 US-08-486- Sequence 16, Applicati	2.42e-53
38	725	67.3	138	2 US-08-508- Sequence 16, Applicati	2.42e-53
39	725	67.3	138	3 US-09-120- Sequence 16, Applicati	2.42e-53
40	725	67.3	138	2 US-08-848- Sequence 16, Applicati	2.42e-53
41	725	67.3	138	3 US-08-581- Sequence 4, Applicatio	2.42e-53
42	682	63.3	136	4 PCT-US96-0 Sequence 6, Applicatio	1.64e-49
43	682	63.3	137	2 US-08-893- Sequence 4, Applicatio	1.64e-49
44	682	63.3	137	2 US-08-306- Sequence 4, Applicatio	1.64e-49
45	676	62.7	168	2 US-08-508- Sequence 46, Applicati	5.61e-49

ALIGNMENTS

RESULT 1
ID PCT-US95-04636-2 STANDARD: PRT: 156 AA.
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DT

Sequence 2, Application PC/TUS9504636
Sequence 2, Application PC/TUS9504636
GENERAL INFORMATION:
APPLICANT:

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii(text)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04636
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 156 AA; 16560 MW; 98948 CN;

Query Match 100.0%; Score 1078; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.93e-85;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC	APPLICATION NUMBER: US 07/963,308
CC	FILING DATE: 16-OCTOBER-1992
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Vincent, Matthew P.
CC	REGISTRATION NUMBER: 36,709
CC	REFERENCE/DOCKET NUMBER: MIV-071.09
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (617) 832-1000
CC	TELEFAX: (617) 832-7000
CC	INFORMATION FOR SEQ ID NO: 2:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 156 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 156 AA; 16560 MW; 98948 CN;
CC	Query Match 100.0%; Score 1078; DB 2; Length 156;
CC	Best Local Similarity 100.0%; Pred. NO. 4,93e-85;
CC	Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps
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QY	1 MDPAAAGSSMEPSADWLATAAARGVEEVALLEAVALPNAPNSYGRRPDIQVMMWGSARVA 60
DB	61 ELLLLHGAEPNCADPATLTPRVHDAAREGFTLTVLHRAAGARLDVRDAGRLPVDLAE 120
QY	61 ELLLLHGAEPNCADPATLTPRVHDAAREGFTLTVLHRAAGARLDVRDAGRLPVDLAE 120
DB	121 LGRHVARVYLRRAAGTGRGNSHARIDAAEGPSDIPD 156
QY	121 LGRHVARVYLRRAAGTGRGNSHARIDAAEGPSDIPD 156
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AC	
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DE	Sequence 2, Application US/08627610
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CC	Sequence 2, Application US/08627610
CC	Patent No. 5919997
CC	GENERAL INFORMATION:
CC	APPLICANT: Beach, David H.
CC	APPLICANT: Serrano, Manuel
CC	APPLICANT: Depinho, Ronald A.
CC	TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
CC	TITLE OF INVENTION: Regulation
CC	NUMBER OF SEQUENCES: 13
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: LAHIVE & COCKFIELD
CC	STREET: 60 State Street
CC	CITY: Boston
CC	STATE: MA
CC	COUNTRY: USA
CC	ZIP: 02109
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: ASCII(text)
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/627,610
CC	FILING DATE: 04-APR-1996
CC	CLASSIFICATION: 800
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Vincent, Matthew P.
CC	REGISTRATION NUMBER: 36,709
CC	REFERENCE/DOCKET NUMBER: CSI-001CP6
CC	TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (617) 227-7400
 CC TELEFAX: (617) 227-5941
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 156 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 156 AA; 16560 MW; 98948 CN;
 Query Match 100.0%; Score 1078; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4,938-85;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 MDPAGSSMEPSADWLATAAARGVEEYRALLLEAVALPNAPNSYGRRPITQVMMGSAVA 60
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
 Db 121 LGHRDVARYLRAAGTGRGSHARIDAAEGPSDIPD 156
 QY 121 LGHRDVARYLRAAGTGRGSHARIDAAEGPSDIPD 156
 RESULT 6
 ID US-08-480-810-2 STANDARD; PRT; 156 AA.
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 AC xxxxxx
 DT
 DE Sequence 2, Application US/08480810
 XX
 CC Sequence 2, Application US/08480810
 CC Patent No. 5801236
 CC GENERAL INFORMATION:
 CC APPLICANT: Kamb, Alexander
 CC TITLE OF INVENTION: MTS1 GENE
 CC NUMBER OF SEQUENCES: 36
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 CC STREET: 1201 New York Avenue, Suite 1000
 CC CITY: Washington
 CC STATE: DC
 CC COUNTRY: USA
 CC ZIP: 20005
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/480,810
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/03316
 CC FILING DATE: 17-MAR-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/251,938
 CC FILING DATE: 01-JUN-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/215,087
 CC FILING DATE: 18-MAR-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/215,086
 CC FILING DATE: 18-MAR-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/227,369
 CC FILING DATE: 14-APR-1994

CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/214,582
 CC FILING DATE: 18-MAR-1994
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Ihnen, Jeffrey L.
 CC REGISTRATION NUMBER: 28,957
 CC REFERENCE/DOCKET NUMBER: 24884-109348
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-962-4810
 CC TELEFAX: 202-962-8300
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 156 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 156 AA; 16532 MW; 98534 CN;
 Query Match 99.0%; Score 1067; DB 1; Length 156;
 Best Local Similarity 98.7%; Pred. No. 4,848-84;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MDPAGSSMEPSADWLATAAARGVEEYRALLLEAVALPNAPNSYGRRPITQVMMGSAVA 60
 QY 1 MDPAGSSMEPSADWLATAAARGVEEYRALLLEAVALPNAPNSYGRRPITQVMMGSAVA 60
 Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
 QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
 Db 121 LGHRDVARYLRAAGTGRGSHARIDAAEGPSDIPD 156
 QY 121 LGHRDVARYLRAAGTGRGSHARIDAAEGPSDIPD 156
 RESULT 7
 ID US-08-486-047-2 STANDARD; PRT; 156 AA.
 XX
 AC xxxxxx
 DT
 DE Sequence 2, Application US/08486047
 XX
 CC Sequence 2, Application US/08486047
 CC Patent No. 5994095
 CC GENERAL INFORMATION:
 CC APPLICANT: Kamb, Alexander
 CC TITLE OF INVENTION: MTS2 GENE
 CC NUMBER OF SEQUENCES: 36
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 CC STREET: 1201 New York Avenue, Suite 1000
 CC CITY: Washington
 CC STATE: DC
 CC COUNTRY: USA
 CC ZIP: 20005
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/486,047
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/03316
 CC FILING DATE: 17-MAR-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/251,938
 CC FILING DATE: 01-JUN-1994
 CC PRIOR APPLICATION DATA:

CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/487,033
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/03316
CC FILING DATE: 17-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348-C
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 156 AA; 16532 MW; 98534 CN;

Query Match 99.0%; Score 1067; DB 1; Length 156;
Best Local Similarity 98.7%; Pred. No. 4.84e-84;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 MEPAAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSYGRPIQVMMGSAVA 60
Qy 1 MDPAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSYGRPIQVMMGSAVA 60
Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLLHAGARLDVDRDANGRLPVDLAE 120
Qy 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLLHAGARLDVDRDANGRLPVDLAE 120
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XX
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DT
XX
DE Sequence 2, Application US/08508735

XX Sequence 2, Application US/08508735
CC Patent No. 5843756
CC GENERAL INFORMATION:
CC APPLICANT: Stone, Steven
CC APPLICANT: Jiang, Ping
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
CC NUMBER OF SEQUENCES: 47
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/508,735
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US to be assigned
CC FILING DATE: 07-JUN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/03316
CC FILING DATE: 17-MAR-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4848
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 156 AA; 16532 MW; 98534 CN;

Query Match 99.0%; Score 1067; DB 2; Length 156;
Best Local Similarity 98.7%; Pred. No. 4.84e-84;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 MEPAAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSYGRPIQVMMGSAVA 60
Qy 1 MDPAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSYGRPIQVMMGSAVA 60
Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLLHAGARLDVDRDANGRLPVDLAE 120
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Qy 121 LGHRDVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156

RESULT 11
ID US-09-120-130-2 STANDARD; PRT; 156 AA.
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AC xxxxxx
XX
DT
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DE Sequence 2, Application US/09120130
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DE Sequence 2, Application US/09120130

WQSRH
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:35:12 2000; MasPar time 11.77 Seconds
625.481 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pep
Perfect Score: 1078
Sequence: 1 MDPAGSMPEPSADWLATAA.....TRGSNHRIDAAEGPSDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir63
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 43.845; Variance 94.938; scale 0.462

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Result No.	Score	Query Match	Description	ID	
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2	729	67.6	pl5INK4b - mouse	130	1.59e-110
3	725	67.3	CDK4 inhibitor p14(IN	138	9.09e-110
4	663	61.5	pl5INK4a - mouse	167	4.46e-98
5	353	32.7	cyclin-dependent kina	164	3.82e-41
6	341	31.6	CDK4/CDK6 inhibitor p	166	5.04e-39
7	338	31.4	cyclin-dependent kina	166	1.70e-38
8	300	27.8	CDK6 inhibitor p18 -	168	7.29e-32
9	292	27.1	CDK4/CDK6 inhibitor p	168	1.75e-30
10	284	26.3	gene pl5INK4B protein	41	4.14e-29
11	181	16.8	ankyrin 2, neuronal 1	3924	3.58e-12
12	174	16.1	ankyrin 1, erythrocyt	1856	4.30e-11
13	174	16.1	ankyrin 1, erythrocyt	1880	4.30e-11
14	174	16.1	ankyrin 1, erythrocyt	1881	4.30e-11
15	173	16.0	ankyrin, erythrocyte	1848	6.11e-11
16	173	16.0	ankyrin - mouse	1862	6.11e-11
17	165	15.3	ankyrin 3, long splic	4377	1.00e-09
18	160	14.8	ankyrin-related prote	2	5.64e-09
19	160	14.8	ankyrin-related unc-4	2	5.64e-09
20	160	14.8	elegans ankyrin-relat	2	5.64e-09
21	160	14.8	ankyrin-related unc-4	2	5.64e-09
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23	152	14.1	ankyrin - fruit fly (2	8.61e-08

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Db	78	ATLTPRVHDAAREGFDTLVVLRHAGARLDVRDANGRLPVDLAEERGHGRDVGAGLYRTATG	137	
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TITLE		p16INK4a - mouse		
ORGANISM		#formal_name Mus sp. #common_name mouse		
DATE		26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change		
ACCESSIONS		I58352		
REFERENCE		I58352		
#authors		Trono, D.; Richter, K.H.; Walker, C.; Beach, D.; Sherr, C.J.; Serrano, M.		
#journal		Oncogene (1995) 11:635-645		
#title		Cloning and characterization of murine p16INK4a and p15INK4b genes.		
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Matches		91;	Conservative 20;	Mismatches 14; Indels 1; Gaps 1;
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QY	129	YLRAAA	134	
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ORGANISM		#formal_name Homo sapiens #common_name man		
DATE		08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change		
ACCESSIONS		A57378		
REFERENCE		A57378		
#authors		Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.		
#journal		Mol. Cell. Biol. (1995) 15:2682-2688		
#title		Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to p16(ink4).		
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13-Aug-1999
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#authors   Chan, W.
#submission submitted to the EMBL Data Library, September 1993
#accession S37431
#status    Preliminary
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#cross-references EMBL:Z26634; NID:9406287; PIDN:CAA81387.1;
               PID:9406288

REFERENCE  A39643
#authors   Otto, F.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
#journal   J. Cell Biol. (1991) 114:241-253
#title     Isolation and characterization of cDNAs encoding human brain
           ankyrins reveal a family of alternatively spliced genes.
#cross-references MUID:91302466
#accession  A39643
#status    Preliminary
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#cross-references EMBL:X56958
               A40334
#authors   Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.;
           Sahr, K.E.; Lux, S.E.; Ward, D.C.; Forget, B.G.
#journal   Genomics (1991) 10:858-866
#title     Isolation and chromosomal localization of a novel
           nonerythroid ankyrin gene.
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#accession  A40334
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#authors   Chan, W.; Kordeli, E.; Bennett, V.
#journal   J. Cell Biol. (1993) 123:1463-1473
#title     440-kD ankyrinB: structure of the major developmentally
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#cross-references MUID:94075409
#accession  A49462
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#cross-references EMBL:Z26634; NID:9406287; PIDN:CAA81387.1;
               PID:9406288

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#keywords      alternative splicing
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               #product ankyrin 2, short form #status predicted #label
               MAV

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96-128     #domain ankyrin repeat homology #label AN02\
129-161    #domain ankyrin repeat homology #label AN03\
162-190    #domain ankyrin repeat homology #label AN04\
191-223    #domain ankyrin repeat homology #label AN05\
232-264    #domain ankyrin repeat homology #label AN06\
265-297    #domain ankyrin repeat homology #label AN07\
298-330    #domain ankyrin repeat homology #label AN08\
331-363    #domain ankyrin repeat homology #label AN09\
364-396    #domain ankyrin repeat homology #label AN10\

DATE      06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
13-Aug-1999
ACCESSIONS S37431; A39643; B39643; A40334; A49462; S14533; S14569
REFERENCE  S37431
#authors   Chan, W.
#submission submitted to the EMBL Data Library, September 1993
#accession S37431
#status    Preliminary
#molecule_type mRNA
#residues  1-3924 #label CHA
#cross-references EMBL:Z26634; NID:9406287; PIDN:CAA81387.1;
               PID:9406288

REFERENCE  A39643
#authors   Otto, F.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
#journal   J. Cell Biol. (1991) 114:241-253
#title     Isolation and characterization of cDNAs encoding human brain
           ankyrins reveal a family of alternatively spliced genes.
#cross-references MUID:91302466
#accession  A39643
#status    Preliminary
#molecule_type mRNA
#residues  1-1443,3585-3924 #label OTT
#cross-references EMBL:X56958
               A40334
#authors   Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.;
           Sahr, K.E.; Lux, S.E.; Ward, D.C.; Forget, B.G.
#journal   Genomics (1991) 10:858-866
#title     Isolation and chromosomal localization of a novel
           nonerythroid ankyrin gene.
#cross-references MUID:92009921
#accession  A40334
#molecule_type DNA
#residues  463-474, 'PE', 477-495 #label TSE
#cross-references GB:M37133; NID:9178647; PIDN:AAA62828.1; PID:9178648
               A49462
#authors   Chan, W.; Kordeli, E.; Bennett, V.
#journal   J. Cell Biol. (1993) 123:1463-1473
#title     440-kD ankyrinB: structure of the major developmentally
           regulated domain and selective localization in unmyelinated
           axons.
#cross-references MUID:94075409
#accession  A49462
#status    Preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues  1-3924 #label RES
#cross-references EMBL:Z26634; NID:9406287; PIDN:CAA81387.1;
               PID:9406288

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#gene      GDB:ANK2
#map_position 4q25-q27
#classification #superfamily ankyrin; ankyrin repeat homology
#keywords      alternative splicing
#feature       2-3924
               #product ankyrin 2, long form #status predicted #label
               MAV
               #product ankyrin 2, short form #status predicted #label
               MAV

63-95      #domain ankyrin repeat homology #label AN01\
96-128     #domain ankyrin repeat homology #label AN02\
129-161    #domain ankyrin repeat homology #label AN03\
162-190    #domain ankyrin repeat homology #label AN04\
191-223    #domain ankyrin repeat homology #label AN05\
232-264    #domain ankyrin repeat homology #label AN06\
265-297    #domain ankyrin repeat homology #label AN07\
298-330    #domain ankyrin repeat homology #label AN08\
331-363    #domain ankyrin repeat homology #label AN09\
364-396    #domain ankyrin repeat homology #label AN10\

397-429    #domain ankyrin repeat homology #label AN11\
430-462    #domain ankyrin repeat homology #label AN12\
463-495    #domain ankyrin repeat homology #label AN13\
496-528    #domain ankyrin repeat homology #label AN14\
529-561    #domain ankyrin repeat homology #label AN15\
562-594    #domain ankyrin repeat homology #label AN16\
595-627    #domain ankyrin repeat homology #label AN17\
628-660    #domain ankyrin repeat homology #label AN18\
661-693    #domain ankyrin repeat homology #label AN19\
694-726    #domain ankyrin repeat homology #label AN20\
727-759    #domain ankyrin repeat homology #label AN21\
760-792    #domain ankyrin repeat homology #label AN22\
793-825    #domain ankyrin repeat homology #label AN23\
SUMMARY    #length 3924 #molecular-weight 430340 #checksum 3664

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Matches 48; Conservative 20; Mismatches 53; Indels 5; Gaps 4;

Db 471 AARAGQVEVYRCILRNALVDAREREQPLHIAASRLGKTEIVQLLOHMAHPDAATNG 530
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 20 AAR-GRVEEVRALEVALPNAPNSYGRPIQVM-MXGSARVAELLLHGAEPNCADPAT 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 531 YT-PLHISAREGOVDVASVLEAGAAHSLATKKGFTPLHVAAYGSLDVAKLLQRRAAA 589
   | | | : |||| : | | | | | | | | | | | | | | | | | | | | | | | | |
QY 78 LTRPVHDAREGEFLDTLVLRHAGARLDVDRDANGRLPVDLAELGHRDVARYL--RAAG 135
   | | | : |||| : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 590 DSAGKN 595
   : | |
QY 136 GTRGSN 141

RESULT 12
ENTRY   B35049
TITLE   ankyrin 1, erythrocyte splice form 3 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS      ankyrin 2.2, erythrocyte
ORGANISM      #formal_name Homo sapiens #common_name man
DATE          17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change
10-Jul-1998
ACCESSIONS B35049
REFERENCE  A35049
#authors   Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.;
           Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
#title     cDNA sequence for human erythrocyte ankyrin.
#cross-references MUID:90175370
#accession  B35049
#status    preliminary
#molecule_type mRNA
#residues  1-1856 #label LAM

GENETICS
#gene      GDB:ANK1; ANK
#map_position 8p11.2-8p11.2
#classification #superfamily ankyrin; ankyrin repeat homology
#keywords      alternative splicing
#feature       2-1856
               #product ankyrin 1, erythrocyte form 3 #status predicted
               #label MAV
               #product ankyrin 2.2, erythrocyte #status predicted
               #label MA2\
               #domain ankyrin repeat homology #label AN01\
               #domain ankyrin repeat homology #label AN02\
               #domain ankyrin repeat homology #label AN03\
               #domain ankyrin repeat homology #label AN04\
               #domain ankyrin repeat homology #label AN05\
               #domain ankyrin repeat homology #label AN06\
               #domain ankyrin repeat homology #label AN07\
               #domain ankyrin repeat homology #label AN08\
               #domain ankyrin repeat homology #label AN09\
               #domain ankyrin repeat homology #label AN10\
               #domain ankyrin repeat homology #label AN11\

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403-435      #domain ankyrin repeat homology #label AN12\
436-468      #domain ankyrin repeat homology #label AN13\
469-501      #domain ankyrin repeat homology #label AN14\
502-534      #domain ankyrin repeat homology #label AN15\
535-567      #domain ankyrin repeat homology #label AN16\
568-600      #domain ankyrin repeat homology #label AN17\
601-633      #domain ankyrin repeat homology #label AN18\
634-666      #domain ankyrin repeat homology #label AN19\
667-699      #domain ankyrin repeat homology #label AN20\
700-732      #domain ankyrin repeat homology #label AN21\
733-765      #domain ankyrin repeat homology #label AN22\
766-798      #domain ankyrin repeat homology #label AN23\
SUMMARY      #length 1856 #molecular-weight 203445 #checksum 6521

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Best Local Similarity 39.0%; Pred. No. 4.30e-11;
Matches 46; Conservative 16; Mismatches 50; Indels 6; Gaps 6;

Db 507 LHIAAREGHVETVLLALLEKEASQACMTKGGFTPLHVAAYKGVKRVVAELLERDAHPNAG 566
QY 16 LATAAARGVEEVRALLEVALPNAPNSYGRRIQVMM-GSARVAELLHGAEPNCAD 74

Db 567 KNGLT-PLHVAHHNNLDIVKLLPRGGSP-HSP-ANNGYTPLHIAAKQNOVEVARSL 621
QY 75 PATLTPVHDAAREGFLDTL-VVLHAGARLDVDRDAW-GRLPVDLAELGHEDVARYL 130

RESULT 13
ENTRY      SJHUK      #type complete
TITLE      ankyrin 1, erythrocyte splice form 2 - human
ALTERNATE_NAMES      ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS      ankyrin 2.2
ORGANISM      #formal_name Homo sapiens #common_name man
DATE      27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change
04-Sep-1998

ACCESSIONS      A35049
REFERENCE      A35049
#authors      Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.;
#journal      Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
#title      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
#cross-references      cDNA sequence for human erythrocyte ankyrin.
#accession      A35049
#status      preliminary
#molecule_type      mRNA
#residues      1-1880 #label LAM
#cross-references      GB:M28880

GENETICS
#gene      GDB:ANK1; ANK
#cross-references      GDB:118737; OMIM:182900
#map_position      9p11.2-9p11.2
CLASSIFICATION      #superfamily ankyrin; ankyrin repeat homology
KEYWORDS      alternative splicing; cytoskeleton
FEATURE
2-1880      #product ankyrin 1, erythrocyte form 2 #status predicted
#label MA1\
2-1513,1676-1880      #product ankyrin 2.2, erythrocyte #status predicted
#label MA2\
44-76      #domain ankyrin repeat homology #label AN01\
77-109      #domain ankyrin repeat homology #label AN02\
110-142      #domain ankyrin repeat homology #label AN03\
143-171      #domain ankyrin repeat homology #label AN04\
172-204      #domain ankyrin repeat homology #label AN05\
205-237      #domain ankyrin repeat homology #label AN06\
238-270      #domain ankyrin repeat homology #label AN07\
271-303      #domain ankyrin repeat homology #label AN08\
304-336      #domain ankyrin repeat homology #label AN09\
337-369      #domain ankyrin repeat homology #label AN10\
370-402      #domain ankyrin repeat homology #label AN11\
403-435      #domain ankyrin repeat homology #label AN12\
436-468      #domain ankyrin repeat homology #label AN13\
469-501      #domain ankyrin repeat homology #label AN14\
502-534      #domain ankyrin repeat homology #label AN15\

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535-567      #domain ankyrin repeat homology #label AN16\
568-600      #domain ankyrin repeat homology #label AN17\
601-633      #domain ankyrin repeat homology #label AN18\
634-666      #domain ankyrin repeat homology #label AN19\
667-699      #domain ankyrin repeat homology #label AN20\
700-732      #domain ankyrin repeat homology #label AN21\
733-765      #domain ankyrin repeat homology #label AN22\
766-798      #domain ankyrin repeat homology #label AN23\
SUMMARY      #length 1880 #molecular-weight 206066 #checksum 6968

Query Match      16.1%; Score 174; DB 2; Length 1880;
Best Local Similarity 39.0%; Pred. No. 4.30e-11;
Matches 46; Conservative 16; Mismatches 50; Indels 6; Gaps 6;

Db 507 LHIAAREGHVETVLLALLEKEASQACMTKGGFTPLHVAAYKGVKRVVAELLERDAHPNAG 566
QY 16 LATAAARGVEEVRALLEVALPNAPNSYGRRIQVMM-GSARVAELLHGAEPNCAD 74

Db 567 KNGLT-PLHVAHHNNLDIVKLLPRGGSP-HSP-ANNGYTPLHIAAKQNOVEVARSL 621
QY 75 PATLTPVHDAAREGFLDTL-VVLHAGARLDVDRDAW-GRLPVDLAELGHEDVARYL 130

RESULT 14
ENTRY      SJHUK      #type complete
TITLE      ankyrin 1, erythrocyte splice form 1 - human
ALTERNATE_NAMES      ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS      ankyrin 2.2
ORGANISM      #formal_name Homo sapiens #common_name man
DATE      30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
22-Jun-1999

ACCESSIONS      S08275; A33219; PC2220; A35443
REFERENCE      S08275
#authors      Lux, S.E.; John, K.M.; Bennett, V.
#journal      Nature (1990) 344:36-42
#title      Analysis of cDNA for human erythrocyte ankyrin indicates a
repeated structure with homology to tissue-differentiation
and cell-cycle control proteins.
#cross-references      MUID:90158830
#accession      S08275
#molecule_type      mRNA
#residues      1-1881 #label LUI
#cross-references      EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702
#accession      A33219
#molecule_type      protein
#residues      2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30; 733-749, 'A', 751-753;
828-833, 'X', 835-855, 'X', 857-859, 'XX', 862-871; 959-1003;
1106-1120, 'XX', 1123-1128; 1149-1172; 1282-1285, 'E',
1287-1288; 1307-1332; 1345-1365, 'X', 1367; 1383-1427;
1601-1630; 1686-1698, 'D', 1700; 1763-1772 #label LUX
#note      845-Arg and 1392-thr were also found
PC2220
#authors      Hermann, J.; Barel, M.; Frade, R.
#journal      Biochem. Biophys. Res. Commun. (1994) 204:453-460
#title      Human erythrocyte ankyrin, a cytoskeleton component,
generates the p57 membrane proteinase which cleaves C3, the
third component of complement.
#cross-references      MUID:95071348
#accession      PC2220
#molecule_type      protein
#residues      910-929 #label HER
REFERENCE      A35443
#authors      Davis, L.H.; Bennett, V.
#journal      J. Biol. Chem. (1990) 265:10589-10596
#title      Mapping the binding sites of human erythrocyte ankyrin for
the anion exchanger and spectrin.
#cross-references      MUID:90285190
#accession      A35443
#molecule_type      protein
#residues      'X', 5, 'X', 7-12; 403-417, 'X', 419-422, 'H', 424, 'IQ', 797-800,
'L', 802-814; 862-863, 'X', 865-877; 'X', 899-901, 'T',
903-909, 'X', 911-912 #label DAV

GENETICS

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#gene GDB:ANK1; ANK
##cross-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing; phosphoprotein
FEATURE
2-1881
#product ankyrin 1, erythrocyte form 1 #status predicted
#label MAT1\
#label MAT2\
2-1512,1675-1881
#product ankyrin 2.2, erythrocyte #status predicted
#label MAT2\
#domain 89K #status predicted #label DOM1\
#region anion exchange protein binding\
#domain ankyrin repeat homology #label AN01\
#domain ankyrin repeat homology #label AN02\
#domain ankyrin repeat homology #label AN03\
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#region spectrin binding\
#domain 55K #status predicted #label DOM3
#length 1881 #molecular-weight 206275 #checksum 2619
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Best Local Similarity 39.0%; Pred. No. 4.30e-11;
Matches 46; Conservative 16; Mismatches 50; Indels 6; Gaps 6;
Db 507 LHIAAREGHVETVYALAEKESQACMTKGGFTPLHVAAYKGVKRVLAELLEDHAPNAAAG 566
QY 16 LATAAARGVEEVRALEVALPNAPNSYGRPIQVMM-GSARVAELLLHGAEPNCAD 74
Db 567 KNGLT-PLHAVHNNLDIVKLLPRGGSP-HSP-ANWGYTTPHIAKONQVEVARSL 621
QY 75 PATLTRPVHDAAREGFDTL-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARYL 130
#cross-references MIM:93252825
#accession S3771
#status preliminary
#molecule_type mRNA
#residues 1-1848 #label BIR
##cross-references EMBL:X69063; NID:g311816; PIDN:CAA48801.1;
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PID:g311817
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing
FEATURE
48-80
81-113
114-146
147-175
176-208
209-241
242-274
275-307
308-340
341-373
374-406
407-439
440-472
473-505
506-538
539-571
572-604
605-637
638-670
671-703
704-736
737-769
770-802
SUMMARY
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Best Local Similarity 38.1%; Pred. No. 6.11e-11;
Matches 45; Conservative 17; Mismatches 50; Indels 6; Gaps 6;
Db 511 LHIAAREGHVDTALAEKESQACMTKGGFTPLHVAAYKGVKRVLAELLEDHAPNAAAG 570
QY 16 LATAAARGVEEVRALEVALPNAPNSYGRPIQVMM-GSARVAELLLHGAEPNCAD 74
Db 571 KNGLT-PLHAVHNNLDIVKLLPRGGSP-HSP-ANWGYTTPHIAKONQVEVARSL 625
QY 75 PATLTRPVHDAAREGFDTL-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARYL 130
Search completed: Thu Jul 20 08:35:26 2000
Job time : 14 secs.
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W P E R E H

(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:35:43 2000; MasPar time 7.46 Seconds
Tabular output not generated. 637.235 Million cell updates/sec

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pap
Perfect Score: 1078
Sequence: 1 MDPAGSMSEPSADWLATAA.....TRGSNHRIDAEGPSDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 44.859; Variance 85.215; scale 0.526

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1067	99.0	156	1	CDN2_HUMAN CYCLIN-DEPENDENT KINASE	1.98e-199
2	729	67.6	130	1	CDN5_MOUSE CYCLIN-DEPENDENT KINASE	6.89e-126
3	725	67.3	138	1	CDN5_HUMAN CYCLIN-DEPENDENT KINASE	5.00e-125
4	720	66.8	130	1	CDN5_RAT CYCLIN-DEPENDENT KINASE	5.94e-124
5	663	61.5	167	1	CDN2_MOUSE CYCLIN-DEPENDENT KINASE	9.94e-112
6	575	53.3	171	1	CDN2_MONDO CYCLIN-DEPENDENT KINASE	5.27e-93
7	364	33.8	166	1	CDN7_HUMAN CYCLIN-DEPENDENT KINASE	3.10e-49
8	341	31.6	166	1	CDN7_MOUSE CYCLIN-DEPENDENT KINASE	1.29e-44
9	300	27.8	168	1	CDN6_HUMAN CYCLIN-DEPENDENT KINASE	1.72e-36
10	292	27.1	168	1	CDN6_MOUSE CYCLIN-DEPENDENT KINASE	6.33e-35
11	181	16.8	1839	1	ANKC_HUMAN ANKYRIN, BRAIN VARIANT	3.37e-14
12	181	16.8	3924	1	ANKB_HUMAN ANKYRIN, BRAIN VARIANT	3.37e-14
13	174	16.1	1880	1	ANKI_HUMAN ANKYRIN R (ANKYRINS 2)	5.58e-13
14	173	16.0	1862	1	ANKL_MOUSE ANKYRIN	8.30e-13
15	143	13.3	1964	1	NTC4_MOUSE NEUROGENIC LOCUS NOTCH	8.65e-08
16	141	13.1	1431	1	DAPK_HUMAN DEATH-ASSOCIATED PROTEIN	1.81e-07
17	136	12.6	323	1	ANKH_CHRYI ANKYRIN HOMOLOG PRECURSOR	1.13e-06
18	128	11.9	2318	1	NTC3_MOUSE NEUROGENIC LOCUS NOTCH	1.99e-05
19	126	11.7	2703	1	NOTC_DRONE NEUROGENIC LOCUS NOTCH	4.03e-05
20	124	11.5	2531	1	NTC1_RAT NEUROGENIC LOCUS NOTCH	8.10e-05
21	123	11.4	2437	1	NOTC_BRARE NEUROGENIC LOCUS NOTCH	1.15e-04
22	123	11.4	2444	1	NTC1_HUMAN NEUROGENIC LOCUS NOTCH	1.15e-04
23	123	11.4	2524	1	NOTC_XENLA NEUROGENIC LOCUS NOTCH	1.15e-04

24	122	11.3	414	1	GABD_MOUSE GA BINDING PROTEIN BET	1.62e-04
25	119	11.0	571	1	GLS1_CAEEL PUTATIVE GLUTAMINASE D	4.54e-04
26	119	11.0	679	1	RN5A_MOUSE 2-5A-DEPENDENT RIBONUC	4.54e-04
27	119	11.0	2531	1	NTC1_MOUSE NEUROGENIC LOCUS NOTCH	4.54e-04
28	117	10.9	227	1	PHLB_SERLI PHLB PROTEIN PRECURSOR	8.94e-04
29	118	10.9	347	1	GABC_MOUSE GA BINDING PROTEIN BET	6.37e-04
30	118	10.9	382	1	GABB_MOUSE GA BINDING PROTEIN BET	6.37e-04
31	117	10.9	677	1	SKD3_MOUSE SKD3 PROTEIN	8.94e-04
32	115	10.7	347	1	GABC_HUMAN GA BINDING PROTEIN BET	1.75e-03
33	115	10.7	383	1	GABB_HUMAN GA BINDING PROTEIN BET	1.75e-03
34	114	10.6	1401	1	LATA_LATMA ALPHA-LATROTOXIN PRECU	2.45e-03
35	111	10.3	248	1	FNRL_RHOSH TRANSCRIPTIONAL ACTIVA	6.59e-03
36	109	10.1	231	1	YZ82_MYCTU HYPOTHETICAL 24.0 KD P	1.27e-02
37	108	10.0	172	1	YB13_FOPDM HYPOTHETICAL BANHI-ORF	1.75e-02
38	108	10.0	188	1	YOAB_ECOLI HYPOTHETICAL 20.8 KD P	1.75e-02
39	108	10.0	457	1	YE07_MYCTU HYPOTHETICAL 48.5 KD P	1.75e-02
40	105	9.7	1083	1	YIL2_YEAST HYPOTHETICAL 123.6 KD	4.57e-02
41	104	9.6	446	1	BCL3_HUMAN B-CELL LYMPHOMA 3-ENCO	6.26e-02
42	101	9.4	653	1	EGLN_MOUSE ENDOGLIN PRECURSOR (CE	1.60e-01
43	100	9.3	703	1	ULI7_HSV11 PROTEIN UL17	2.17e-01
44	100	9.3	740	1	Y050_HUMAN HYPOTHETICAL PROTEIN K	2.17e-01
45	100	9.3	2156	1	ORP1_HUMAN OXYGEN-REGULATED PROTE	2.17e-01

ALIGNMENTS

RESULT	ID	CDN2_HUMAN	STANDARD;	PRT;	156 AA.
AC	P42771	Q15191			
DT	01-NOV-1995	(Rel. 32, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I)	(P16-INK4A)			
DE	(MULTIPLE TUMOR SUPPRESSOR 1) (MTS1).				
GN	CDKN2A OR CDKN2				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 94081956				
RA	Serrano M., Hannon G.J., Beach D.;				
RT	"A new regulatory motif in cell-cycle control causing specific				
RT	Inhibition of cyclin D/CDK4."				
RL	Nature 366:704-707(1993).				
RN	[2]				
RP	SEQUENCE OF 51-152 FROM N.A.				
RX	MEDLINE; 94204645				
RA	Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,				
RA	Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,				
RA	Skolnick M.H.;				
RT	"A cell cycle regulator potentially involved in genesis of many tumor				
RT	types."				
RL	Science 264:436-440(1994).				
RN	[3]				
RP	SEQUENCE OF 1-20 FROM N.A.				
RX	MEDLINE; 96182088				
RA	Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;				
RT	"Regulation of p16CDKN2 expression and its implications for cell				
RT	immortalization and senescence."				
RL	Mol. Cell. Biol. 16:859-867(1996).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.				
RX	MEDLINE; 98421670				
RA	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;				
RT	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6				
RT	by the tumour suppressor p16INK4a."				
RL	Nature 395:237-243(1998).				
RN	[5]				
RP	REVIEW ON MELANOMA VARIANTS.				
RX	MEDLINE; 96377761				
RA	Dracopoli N.C., Fountain J.W.;				
RT	"CDKN2 mutations in melanoma."				

Cancer Surv. 26:115-132(1996).

[6] REVIEW ON VARIANTS.

RA MEDLINE; 96303699.

RA Smith-Soerensen B., Kovig E.;

RT "CDKN2A (p16INK4a) somatic and germline mutations.";

RL Hum. Mutat. 7:294-303(1996).

[7] VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).

RA MEDLINE; 94338359.

RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;

RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41

RT (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small

RT cell lung carcinomas.";

RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).

[8] VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.

RA MEDLINE; 95078916.

RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,

RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;

RT "Germline p16 mutations in familial melanoma.";

RL Nat. Genet. 8:15-21(1994).

[9] VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.

RA MEDLINE; 95060835.

RA Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,

RA Abraham J.M., Meltzer S.J.;

RT "The MTS1 gene is frequently mutated in primary human esophageal

RT tumors.";

RL Oncogene 9:3737-3741(1994).

[10] VARIANTS.

RA MEDLINE; 95188190.

RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,

RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,

RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;

RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in

RT primary and metastatic lung cancer.";

RL Cancer Res. 55:1448-1451(1995).

[11] VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.

RA MEDLINE; 96121580.

RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,

RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;

RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma

RT kindreds.";

RL Hum. Mol. Genet. 4:1845-1852(1995).

[12] CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.

RA MEDLINE; 95375774.

RA Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,

RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,

RA Dracopoli N.C.;

RT "Mutations associated with familial melanoma impair p16INK4

RT function.";

RL Nat. Genet. 10:114-116(1995).

[13] VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.

RA MEDLINE; 96323259.

RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,

RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,

RA Isseilbacher K.J., Sober A.J., Haber D.A.;

RT "Prevalence of germline mutations in p16, p19ARF, and CDK4 in

RT familial melanoma: analysis of a clinic-based population.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).

[14] VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.

RA MEDLINE; 97472457.

RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,

RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,

RA Bishop D.T., Bishop J.N.;

RT "Germline mutations of the CDKN2 gene in UK melanoma families.";

RL Hum. Mol. Genet. 6:2061-2067(1997).

[15] VARIANTS FAMILIAL MELANOMA.

RA MEDLINE; 98087572.

RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,

RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;

RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone

RT families in France.";

RL Hum. Mol. Genet. 7:209-216(1998).

[16] ERRATUM.

RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,

RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;

RL Hum. Mol. Genet. 7:941-941(1998).

[17] VARIANT PANCREATIC CARCINOMA CYS-146.

RA Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,

RA Lynch J., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;

RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple

RT pancreatic carcinomas.";

RL Hum. Mutat. 12:70-70(1998).

[18] VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.

RA Gretarsdottir S., Olafsdottir G.H., Borg A.;

RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,

RT glioma and carcinoma of the pancreas.";

RL Hum. Mutat. 12:212-212(1998).

CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS

CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE

CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.

CC -!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.

CC -!- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A

CC WIDE RANGE OF TISSUES.

CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE

CC INHIBITORS.

CC -!- SIMILARITY: CONTAINS 4 ANK REPEATS.

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CC -----

DR EMBL; L27211; AAA92554.1; -

DR EMBL; U12820; AAB60645.1; -

DR EMBL; U12818; AAB60645.1; JOINED.

DR EMBL; U12819; AAB60645.1; JOINED.

DR EMBL; S69804; AAD14048.1; -

DR EMBL; X94154; CAA63870.1; -

DR PDB; 1BI7; 16-FEB-99.

DR MIM; 600160; -

DR PFAM; PF00023; ank; 3.

KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;

KW Polymorphism; 3D-structure.

FT DOMAIN 12 141

FT REPEAT 12 43

FT REPEAT 44 75

FT REPEAT 77 109

FT REPEAT 110 141

FT VARIANT 14 14

FT VARIANT 16 16

FT VARIANT 20 20

FT VARIANT 20 20

FT VARIANT 23 23

FT VARIANT 24 24

FT 4 X ANK MOTIF REPEATS.

FT ANK MOTIF 1 (INCOMPLETE).

FT ANK MOTIF 2.

FT ANK MOTIF 3.

FT ANK MOTIF 4.

FT D -> E (IN A BILIARY TRACT TUMOR).

FT /FTID-Var_001408.

FT L -> P (IN A BILIARY TRACT TUMOR AND A

FT FAMILIAL MELANOMA).

FT /FTid-Var_001409.

FT A -> P (IN A LUNG TUMOR AND MELANOMA).

FT /FTid-Var_001410.

FT A -> S (IN A BILIARY TRACT TUMOR).

FT /FTid-Var_001411.

FT G -> D (IN A PANCREAS TUMOR).

FT /FTid-Var_001412.

FT R -> C (IN MELANOMA).

FT /FTid-Var_001413.

```

FT VARIANT 24 24 R -> P (IN FAMILIAL MELANOMA AND
FT MELANOMA).
FT /FTID-VAR_001414.
FT E -> D (IN A BILIARY TRACT TUMOR).
FT VARIANT 26 26 /FTID-VAR_001415.
FT /FTID-VAR_001415.
FT VARIANT 32 32 L -> P (IN FAMILIAL MELANOMA).
FT /FTID-VAR_001416.
FT VARIANT 33 33 E -> D (IN A BILIARY TRACT TUMOR).
...
Note: remainder of annotations omitted.

Query Match 99.0%; Score 1067; DB 1; Length 156;
Best Local Similarity 98.7%; Pred. No. 1.98e-199;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MEPAAGSMPSADWLATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGMSARVA 60
QY 1 MDPAGSMPSADWLATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGMSARVA 60
Db 61 ELLLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLAE 120
QY 61 ELLLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLAE 120
Db 121 LGRDVARYLRAAAGTRGSNHRIDAAREGSPDIP 156
QY 121 LGRDVARYLRAAAGTRGSNHRIDAAREGSPDIP 156

RESULT 2
ID CDN5_MOUSE STANDARD; PRT; 130 AA.
AC P5271.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95380169.
RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RA "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RA Oncogene 11:635-645(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6J X DBA;
RX MEDLINE; 9732242.
RA Malumbres M., de Castro I., Santos J., Melendez B., Manges R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by
RT deletion and de novo methylation with independence of p16INK4a
RT alterations in murine primary T-cell lymphomas.";
RL Oncogene 14:1361-1370(1997).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED UBQUITOUSLY.
CC -1- INDUCTION: BY TGF-BETA.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
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CC -----
DR EMBL; U66085; AAB39833.1;
DR EMBL; U66084; AAB39833.1; JOINED.
DR MGD; MG1:104737; CDKN2B.
DR PFAM; PF00023; ank; 3.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.
FT DOMAIN 5 95 2 X ANK MOTIF REPEATS.
FT REPEAT 5 31 ANK MOTIF 1 (INCOMPLETE).
FT REPEAT 65 95 ANK MOTIF 2.
SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF552BCFF9 CRC64;

Query Match 67.6%; Score 729; DB 1; Length 130;
Best Local Similarity 88.3%; Pred. No. 6.89e-126;
Matches 106; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 10 LATAAARGVETVQLLEAGALPNALNFRGRRPIQVMMGMSAQVAELLHLHGAENPCADP 69
QY 16 LATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGMSARVAELLHLHGAENPCADP 75
Db 70 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVCDAGRLPVDLAEEOGHRIARYLHAATG 129
QY 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLAEELGHRDVARYLRAAG 135

RESULT 3
ID CDN5_HUMAN STANDARD; PRT; 138 AA.
AC P42772.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
DE (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
GN CDKN2B OR MTS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95095079.
RA Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
RA Matera G.A., Xiong Y.;
RT "Growth suppression by p18, a p16INK4a/MTS1- and p14INK4b/MTS2-related
RT CDK6 inhibitor, correlates with wild-type pRb function.";
RL Genes Dev. 8:2939-2952(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94359613.
RA Hannon G.J., Beach D.;
RT "p15INK4b is a potential effector of TGF-beta-induced cell cycle
RT arrest.";
RL Nature 371:257-261(1994).
RN [3]
RP SEQUENCE OF 53-138 FROM N.A.
RX MEDLINE; 94204645.
RA Kamb A., Gius N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
RA Ravtignan S.V., Stockert E., Day R.S. III, Johnson B.E.,
RA Skolnick M.H.;
RT "A cell cycle regulator potentially involved in genesis of many tumor
RT types.";
RL Science 264:436-440(1994).
RN [4]
RP VARIANTS LUNG ADENOCARCINOMA GLO-47 AND VAL-50.
RX MEDLINE; 95188190.
RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,
RA Xiong Y., Beach D.H., Yokota J., Harris C.C.;
RT "Mutations in the p16INK4a/MTS1/CDKN2, p15INK4b/MTS2, and p18 genes in
RT primary and metastatic lung cancer.";
RL Cancer Res. 55:1448-1451(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.

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RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE; 98455510.
RA Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
  Holak T.A.;
RT "Structure of human cyclin-dependent kinase inhibitor p19(INK4d):
  comparison to known ankyrin-repeat-containing structures and
  implications for the dysfunction of tumor suppressor p16(INK4a).";
RT Structure 6:1279-1290(1998).
RL Mol. Cell. Biol. 15:2682-2688(1995).
CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
  INHIBITORS.
CC -!- SIMILARITY: CONTAINS 4 ANK REPEATS.
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DR EMBL; U49399; AAB03772.1; -.
DR EMBL; U40343; AAB18139.1; -.
DR EMBL; U20498; AAB85436.1; -.
DR EMBL; AF061327; AAC27450.1; -.
DR PDB; 1BI8; 16-FEB-99.
DR PDB; 1BD8; 14-OCT-98.
DR MIM; 600927; -.
DR PFAM; PF00023; ank; 3.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure.
FT DOMAIN 7 137 4 X ANK MOTIF REPEATS.
FT REPEAT 7 41 ANK MOTIF 1.
FT REPEAT 42 72 ANK MOTIF 2.
FT REPEAT 73 104 ANK MOTIF 3.
FT REPEAT 105 137 ANK MOTIF 4.
FT CONFLICT 159 159 Q -> P (IN REF. 3).
SQ SEQUENCE 166 AA; 17700 MW; 2FACDLCF56340DC CRC64;

Query Match 33.8%; Score 364; DB 1; Length 166;
Best Local Similarity 49.2%; Pred. No. 3.10e-49;
Matches 61; Conservative 22; Mismatches 39; Indels 2; Gaps 2;

Db 8 AGRLSGAARGDVQVRELLHRELHPDLPALNPFCKTALQVMMFGSPAVALELLKQASPN 67
QY 12 SADWLATAARGVREVRALLE-AVALPNAPNSYGRRPQVMMGSAARVAELLLHGAP 70
Db 68 NYQDTSG-TSPVHDAARTGFLDTLVKLVHVGADVNPDCGTGALPIHLAVOEGHTAVVSFL 126
QY 71 NCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVWDANGRLPVDLAEELGHRDVARYL 130
Db 127 AAES 130
QY 131 RAAA 134

RESULT 8
ID CDN7_MOUSE STANDARD; PRT; 166 AA.
AC Q60773; Q60794;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
GN CDKN2D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL KAPLAN;
RX MEDLINE; 95257948.
RA Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
RT "Novel INK4 proteins, p19 and p18, are specific inhibitors of the

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RT cyclin D-dependent kinases CDK4 and CDK6.";
RL Mol. Cell. Biol. 15:2672-2681(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95257949.
RA Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;
RT "Identification of human and mouse p19, a novel CDK4 and CDK6
  inhibitor with homology to p16ink4.";
RL Mol. Cell. Biol. 15:2682-2688(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE; 98013176.
RA Luh F.Y., Archer S.J., Domaille P.J., Smith B.O., Owen D.,
  Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
  Laue E.D.;
RT "Structure of the cyclin-dependent kinase inhibitor p19Ink4d.";
RL Nature 389:999-1003(1997).
CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
  INHIBITORS.
CC -!- SIMILARITY: CONTAINS 4 ANK REPEATS.
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CC -----
DR EMBL; U19597; AAC52194.1; -.
DR EMBL; U20497; AAB85437.1; -.
DR PDB; 1AP7; 16-SEP-98.
DR MGD; MGI:105387; CDKN2D.
DR PFAM; PF00023; ank; 3.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure.
FT DOMAIN 7 137 4 X ANK MOTIF REPEATS.
FT REPEAT 7 41 ANK MOTIF 1.
FT REPEAT 42 72 ANK MOTIF 2.
FT REPEAT 73 104 ANK MOTIF 3.
FT REPEAT 105 137 ANK MOTIF 4.
FT CONFLICT 17 17 A -> P (IN REF. 2).
SQ SEQUENCE 166 AA; 17894 MW; 9E74F5C23B7EBCB2 CRC64;

Query Match 31.6%; Score 341; DB 1; Length 166;
Best Local Similarity 49.6%; Pred. No. 1.29e-44;
Matches 59; Conservative 19; Mismatches 39; Indels 2; Gaps 2;

Db 9 GDRLSGAARGDVQVRELLHRELHPDLPALNPFCKTALQVMMFGSPAVALELLKQASPN 68
QY 13 ADWLATAARGVREVRALLE-AVALPNAPNSYGRRPQVMMGSAARVAELLLHGAPEN 71
Db 69 VQDASG-TSPVHDAARTGFLDTLVKLVHVGADVNPDCGTGALPIHLAREGHSVVSFL 126
QY 72 CADPATLTPVHDAAREGFLDTLVVLRHAGARLDVWDANGRLPVDLAEELGHRDVARYL 130

RESULT 9
ID CDN6_HUMAN STANDARD; PRT; 168 AA.
AC P42773;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
  KINASE 4 INHIBITOR C) (P18-INK4C).
GN CDKN2C OR CDKN6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthera; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95095079.
RA Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,

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RA Madera G.A., Xiong Y.;
 RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
 RL CDK6 inhibitor, correlates with wild-type pRB function.";
 RN Genes Dev. 8:2939-2952(1994).
 [2]
 RP SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.
 RC TISSUE-BREAST;
 RX MEDLINE: 98300299.
 RA Blais A., Labrie Y., Pouliot F., Lachance Y., Labrie C.;
 RT "Structure of the gene encoding the human cyclin-dependent kinase
 RL inhibitor p18 and mutational analysis in breast cancer";
 RN Biochem. Biophys. Res. Commun. 247:146-153(1998).
 [3]
 RP VARIANT BREAST CANCER PRO-72.
 RX MEDLINE: 96438606.
 RA Lapointe J., Lachance Y., Labrie Y., Labrie C.;
 RT "A p18 mutant defective in CDK6 binding in human breast cancer
 RL cells";
 RN Cancer Res. 56:4586-4589(1996).
 [4]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RX MEDLINE: 98100086.
 RA Venkataramani R., Swaminathan K., Marmorstein R.;
 RT "Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides
 RL insights into ankyrin-like repeat structure/function and
 RN tumor-derived p16INK4 mutations";
 [5]
 RP Nat. Struct. Biol. 5:74-81(1998).
 [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE: 99175088.
 RA Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Malley P., Selby T.,
 RN Tsai M.-D.;
 RT "Tumor suppressor INK4: determination of the solution structure of
 RL p18INK4c and demonstration of the functional significance of loops in
 RN p18INK4c and p16INK4a";
 RT Biochemistry 38:2930-2940(1999).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
 CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
 CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
 CC -1- SUBUNIT: HETERODIMER OF P18 WITH CDK6.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. ALSO
 CC FOUND IN PANCREAS AND HEART.
 CC -1- DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 CC INHIBITORS.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U17074; AAC50074.1; --
 DR EMBL: AF041248; AAC39782.1; --
 DR EMBL: AF041250; AAC39783.1; --
 DR EMBL: AF041249; AAC39783.1; JOINED.
 DR PDB: 1IBB; 13-JAN-99.
 DR PDB: 1BU9; PRELIMINARY.
 DR MIM: 603369; --
 DR PFAM: PF00023; ank; 3.
 KW Cell cycle; Repeat; ANK repeat; Disease mutation; 3D-structure.
 FT DOMAIN 5 135 4 X ANK MOTIF REPEATS.
 FT REPEAT 5 36 ANK MOTIF 1.
 FT REPEAT 37 68 ANK MOTIF 2.
 FT REPEAT 69 101 ANK MOTIF 3.
 FT REPEAT 102 135 ANK MOTIF 4.
 FT VARIANT 72 72
 SQ SEQUENCE 168 AA; 18127 MW; 5D66AFA715186E9A CRC64;

Query Match 27.8%; Score 300; DB 1; Length 168;
 Best Local Similarity 39.6%; Pred. No. 1.72e-36;
 Matches 55; Conservative 35; Mismatches 48; Indels 1; Gaps 1;
 DB 3 EPWGNELASAAARGDLEQLTSLQNNVNVNAQNGFGRTALQVNMKGPNPEIARRLLRGAN 62
 QY 10 EPSADWLATAAARGVEEVRALEVALPNAPNSYGRPIQVNMGSGARVAELLHGAE 69
 DB 63 PDLKRTGFA-VIHDAARAGFLDTLQLEFQADVNIENEGNLPLHLAAKEGHLRVVEF 121
 QY 70 PNCADPATLTPRVDAAREGFLDTLVVLRAGARLDVVDAGRLPVDLAELGHRDVARY 129
 DB 122 LVKHTASNVGHRNHKGDTA 140
 QY 130 LRAAGGTGSGNHARIDAA 148
 RESULT 10
 ID CDN6_MOUSE STANDARD; PRT; 168 AA.
 AC Q60772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
 DE KINASE 4 INHIBITOR C) (P18-INK4C).
 GN CDKN2C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL KAPLAN;
 RX MEDLINE: 95257948.
 RA Hirai H., Rousset M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
 RT "Novel INK4 proteins, p19 and p18, are specific inhibitors of the
 RL cyclin D-dependent kinases CDK4 and CDK6";
 RN Mol. Cell. Biol. 15:2672-2681(1995).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
 CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
 CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
 CC -1- SUBUNIT: HETERODIMER OF P18 WITH CDK6 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 CC INHIBITORS.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U19596; AAC52193.1; --
 DR EMBL: MG1:105388; CDKN2C.
 DR PFAM: PF00023; ank; 3.
 KW Cell cycle; Repeat; ANK repeat.
 FT DOMAIN 5 135 4 X ANK MOTIF REPEATS.
 FT REPEAT 5 36 ANK MOTIF 1.
 FT REPEAT 37 68 ANK MOTIF 2.
 FT REPEAT 69 101 ANK MOTIF 3.
 FT REPEAT 102 135 ANK MOTIF 4.
 SQ SEQUENCE 168 AA; 18066 MW; BC88D5489307E128 CRC64;
 Query Match 27.1%; Score 292; DB 1; Length 168;
 Best Local Similarity 43.08%; Pred. No. 6.33e-35;
 Matches 52; Conservative 29; Mismatches 39; Indels 1; Gaps 1;
 DB 3 EPWGNELASAAARGDLEQLTSLQNNVNVNAQNGFGRTALQVNMKGPNPEIARRLLRGAN 62
 QY 10 EPSADWLATAAARGVEEVRALEVALPNAPNSYGRPIQVNMGSGARVAELLHGAE 69

Db 63 PNLDKGTGFA-VIHDAARAGFLDTQALLERQADVNIENEGNPLHLAAKEGLHPVVEF 121
 Qy 70 PNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVRDANGRLPVDLAELGHRDVARY 129

Db 122 L 122
 Qy 130 L 130

RESULT 11
 ID ANKC_HUMAN STANDARD; PRT; 1839 AA.
 AC Q01485;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)
 DE (FRAGMENT).
 GN ANK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN STEM;
 RX MEDLINE; 91302466.
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and characterization of cDNAs encoding human brain
 RT ankyrins reveal a family of alternatively spliced genes.";
 RL J. Cell Biol. 114:241-253(1991).
 RN [2]
 RP SEQUENCE OF 463-495 FROM N.A.
 RX MEDLINE; 92009921.
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
 RA Lux S.E., Ward D.C., Forget B.G.;
 RT "Isolation and chromosomal localization of a novel nonerythroid
 RT ankyrin gene.";
 RL Genomics 10:858-866(1991).
 CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
 CC SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
 CC BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,
 CC AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
 CC DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
 CC THE CYTOSKELETAL DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC -1- ALTERNATIVE PRODUCTS: THE TWO BRAIN VARIANTS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF GENE ANK2.
 CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
 CC CELLS THROUGHOUT THE BRAIN.
 CC -1- SIMILARITY: CONTAINS 24 ANK REPEATS.
 CC -----
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 CC -----
 DR EMBL; X56958; G29491; -.
 DR EMBL; M37123; AAA62828.1; -.
 DR PIR; S14569; S14569.
 DR PIR; B39643; B39643.
 DR HSP; Q00420; IAWC.
 DR MIM; 106410; -.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PFAM; PF00023; ank; 22.
 DR PFAM; PF00531; death; 1.
 DR PFAM; PF00791; ZU5; 1.
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
 KW Multigene family. 63 792 22 X ANK MOTIF REPEATS.
 FT DOMAIN 63 95
 FT REPEAT 63 95 ANK MOTIF 1.
 FT REPEAT 96 128 ANK MOTIF 2.

FT REPEAT 129 161 ANK MOTIF 3.
 FT REPEAT 162 190 ANK MOTIF 4.
 FT REPEAT 191 231 ANK MOTIF 5.
 FT REPEAT 232 264 ANK MOTIF 6.
 FT REPEAT 265 297 ANK MOTIF 7.
 FT REPEAT 298 330 ANK MOTIF 8.
 FT REPEAT 331 363 ANK MOTIF 9.
 FT REPEAT 364 396 ANK MOTIF 10.
 FT REPEAT 397 429 ANK MOTIF 11.
 FT REPEAT 430 462 ANK MOTIF 12.
 FT REPEAT 463 495 ANK MOTIF 13.
 FT REPEAT 496 528 ANK MOTIF 14.
 FT REPEAT 529 561 ANK MOTIF 15.
 FT REPEAT 562 594 ANK MOTIF 16.
 FT REPEAT 595 627 ANK MOTIF 17.
 FT REPEAT 628 660 ANK MOTIF 18.
 FT REPEAT 661 693 ANK MOTIF 19.
 FT REPEAT 694 726 ANK MOTIF 20.
 FT REPEAT 727 759 ANK MOTIF 21.
 FT REPEAT 760 792 ANK MOTIF 22.
 FT DOMAIN 1451 1535 DEATH DOMAIN.
 FT CONFLICT 475 476
 FT NON_TER 1839 1839 GQ -> PE (IN REF. 2).
 SQ SEQUENCE 1839 AA; 202409 MW; 5C1C1FD3D795A280 CRC64;

Query Match 16.8%; Score 181; DB 1; Length 1839;
 Best Local Similarity 38.1%; Pred. No. 3.37e-14;
 Matches 48; Conservative 20; Mismatches 53; Indels 5; Gaps 4;

Db 471 AARAGOVVVRCLLRNGALVDARAREOTPLHIASRLGKTEIVOLLQHMHPDAATNG 530
 Qy 20 AAR-GRVEEVALLNVALEPNAPNSYGRPIQVW-MGSAARVAELLHLGAEPCADPAT 77
 Db 531 YT-PLHISAREQVDVASVLEAGAAHSLATKKGFTPLHVAAKYGSLDVAKLLQRRAAA 589
 Qy 78 LTRPVHDAAREGFLDTLVVLRAGARLDVRDANGRLPVDLAELGHRDVARYL--RAAAG 135
 Db 590 DSAGKN 595
 Qy 136 GTRGSN 141

RESULT 12
 ID ANKB_HUMAN STANDARD; PRT; 3924 AA.
 AC Q01484; 1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).
 GN ANK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN STEM;
 RX MEDLINE; 94075409.
 RA Chan W., Kordell E., Bennett V.;
 RA "440-KD ankyrinB: structure of the major developmentally regulated
 RA domain and selective localization in unmyelinated axons.";
 RL J. Cell Biol. 123:1463-1473(1993).
 RN [2]
 RP SEQUENCE OF 1-2077 FROM N.A.
 RC TISSUE-BRAIN STEM;
 RX MEDLINE; 91302466.
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
 RA "Isolation and characterization of cDNAs encoding human brain
 RA ankyrins reveal a family of alternatively spliced genes.";
 RL J. Cell Biol. 114:241-253(1991).
 CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
 CC SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
 CC BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,
 CC AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND

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EMBL; X16609; CAA34610.1; -;
EMBL; M28880; AAA51732.1; -;
PIR; S08275; SJHUK.
PIR; A35049; A35049.
HSSP; Q00420; IAWC.
MIM; 182900; -;
PROSITE; PS50017; DEATH_DOMAIN; 1.
PFAM; PF00023; ank; 22.
PFAM; PF00531; death; 1.
PFAM; PF00791; ZU5; 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
Phosphorylation; Lipoprotein; Multigene family; Disease mutation;
Elliptocytosis; Polymorphism.
INIT_MET 0
DOMAIN 1 826 89 KD DOMAIN (ANION EXCHANGE PROTEIN
BINDING DOMAIN).
DOMAIN 827 1381 62 KD DOMAIN (SPECTRIN BINDING
DOMAIN).
DOMAIN 1382 1880 55 KD REGULATORY DOMAIN (REGULATES
THE BINDING OF ANKYRIN TO SPECTRIN
AND THE BAND 3 PROTEIN).
24 X ANK MOTIF REPEATS.
ANK MOTIF 1. 777
ANK MOTIF 2. 31
ANK MOTIF 3. 42
ANK MOTIF 4. 75
ANK MOTIF 5. 108
ANK MOTIF 6. 141
ANK MOTIF 7. 170
ANK MOTIF 8. 203
ANK MOTIF 9. 236
ANK MOTIF 10. 269
ANK MOTIF 11. 302
ANK MOTIF 12. 335
ANK MOTIF 13. 368
ANK MOTIF 14. 401
ANK MOTIF 15. 434
ANK MOTIF 16. 467
ANK MOTIF 17. 500
ANK MOTIF 18. 533
ANK MOTIF 19. 566
ANK MOTIF 20. 599
ANK MOTIF 21. 632
ANK MOTIF 22. 665
ANK MOTIF 23. 698
ANK MOTIF 24. 731
ANK MOTIF 25. 764
ANK MOTIF 26. 777
DEATH DOMAIN.
MISSING (IN ISOFORM 2.2).
H -> D (IN ISOFORM 2.2).
TVEGLEDFSELDVIDYFMKSHDHTSTNP -> ELRGS
GLQPLIEGRGAQIVKRAKLRGKQ (IN A THIRD
ISOFORM).
R -> T.
/FTId-VAR_000595.
V -> I (IN HS).
/FTId-VAR_000596.
R -> H (IN BRUEGGEN).
/FTId-VAR_000597.
V -> A.
/FTId-VAR_000598.
D -> E.
/FTId-VAR_000599.
S -> T.
/FTId-VAR_000600.
E -> D.
/FTId-VAR_000601.

FT VARIANT 1591 1591 D -> N (IN DUESSELDORF).
FT /FTId-VAR_000602.
FT R -> D.
FT VARIANT 1698 1698 /FTId-VAR_000603.
FT A -> S (IN REF. 2).
FT CONFLICT 229 229 V -> I (IN REF. 2).
FT CONFLICT 1545 1545 A -> S (IN REF. 2).
SQ SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFD1CD428 CRC64;
Query Match 16.1%; Score 174; DB 1; Length 1880;
Best Local Similarity 39.0%; Pred. No. 5.58e-13;
Matches 46; Conservative 16; Mismatches 50; Indels 6; Gaps 6;
Db 506 LHIAAREGHVETVALLLEKEASQACMTKGTPLHVAKYGVKRVVAELLRLDRHPNAG 565
Qy 16 LATAARGRVVEVALLLEVALPNAPNSYGRPIQVMMX-GSARVAELLHLGHPNAD 74
Db 566 KNGLT-PLHVAHHNLDIVKLLPRGGSP-HSP-AMNGYTPFLHIAKQNOVEVARSL 620
Qy 75 PATLTPRVHDAAREGFLDTL-VVLHAGARLDVRDAG-GRLPVDLAELGHRDVARYL 130
RESULT 14
ID ANK1_MOUSE STANDARD; PRT; 1862 AA.
AC Q02357;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ANKYRIN.
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-ERYTHROCYTE;
RX MEDLINE; 92345717.
RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
regulatory domain";
RL Mamm. genome 3:281-285(1992).
CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CYTOPLASMIC DOMAIN OF THE ERYTHROCYTE ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
PLASMA MEMBRANE.
CC -1- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 22 ANK REPEATS.

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EMBL; M84756; AAA37236.1; -;
HSSP; Q00420; IAWC.
MGD; MGI:88024; ANK1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PFAM; PF00023; ank; 23.
PFAM; PF00531; death; 1.
PFAM; PF00791; ZU5; 1.
Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
DOMAIN 1 827 89 KD DOMAIN (ANION EXCHANGE PROTEIN
BINDING DOMAIN).
DOMAIN 828 1386 62 KD DOMAIN (SPECTRIN BINDING
DOMAIN).
FT

FT REPEAT 1622 1653 ANK MOTIF 2.
FT REPEAT 1654 1685 ANK MOTIF 3.
FT REPEAT 1688 1719 ANK MOTIF 4.
FT REPEAT 1721 1752 ANK MOTIF 5.
FT REPEAT 1754 1785 ANK MOTIF 6.
FT DISULFID 25 38 BY SIMILARITY.
FT DISULFID 32 48 BY SIMILARITY.
FT DISULFID 50 59 BY SIMILARITY.
FT DISULFID 65 77 BY SIMILARITY.
FT DISULFID 71 100 BY SIMILARITY.
FT DISULFID 102 111 BY SIMILARITY.
FT DISULFID 119 130 BY SIMILARITY.
FT DISULFID 124 140 BY SIMILARITY.
FT DISULFID 142 151 BY SIMILARITY.
FT DISULFID 157 168 BY SIMILARITY.
FT DISULFID 162 177 BY SIMILARITY.
FT DISULFID 179 188 BY SIMILARITY.
FT DISULFID 195 208 BY SIMILARITY.
FT DISULFID 202 217 BY SIMILARITY.
FT DISULFID 219 228 BY SIMILARITY.
FT DISULFID 235 246 BY SIMILARITY.
FT DISULFID 240 259 BY SIMILARITY.
FT DISULFID 261 270 BY SIMILARITY.
FT DISULFID 277 288 BY SIMILARITY.
FT DISULFID 282 297 BY SIMILARITY.
FT DISULFID 299 308 BY SIMILARITY.
FT DISULFID 315 329 BY SIMILARITY.
FT DISULFID 323 338 BY SIMILARITY.
FT DISULFID 340 349 BY SIMILARITY.
FT DISULFID 356 367 BY SIMILARITY.
FT DISULFID 361 376 BY SIMILARITY.
FT DISULFID 378 387 BY SIMILARITY.
FT DISULFID 393 404 BY SIMILARITY.
FT DISULFID 398 415 BY SIMILARITY.
FT DISULFID 417 426 BY SIMILARITY.
FT DISULFID 433 449 BY SIMILARITY.
FT DISULFID 443 458 BY SIMILARITY.
FT DISULFID 460 469 BY SIMILARITY.
FT DISULFID 476 487 BY SIMILARITY.
FT DISULFID 481 496 BY SIMILARITY.
FT DISULFID 498 507 BY SIMILARITY.
FT DISULFID 514 525 BY SIMILARITY.
FT DISULFID 519 534 BY SIMILARITY.
FT DISULFID 536 545 BY SIMILARITY.
FT DISULFID 552 563 BY SIMILARITY.
FT DISULFID 557 572 BY SIMILARITY.
FT DISULFID 574 583 BY SIMILARITY.
FT DISULFID 590 601 BY SIMILARITY.
FT DISULFID 595 610 BY SIMILARITY.
FT DISULFID 612 621 BY SIMILARITY.
FT DISULFID 626 637 BY SIMILARITY.
FT DISULFID 631 646 BY SIMILARITY.
FT DISULFID 648 655 BY SIMILARITY.
FT DISULFID 662 669 BY SIMILARITY.
FT DISULFID 664 674 BY SIMILARITY.
FT DISULFID 676 685 BY SIMILARITY.
FT DISULFID 692 703 BY SIMILARITY.
FT DISULFID 697 712 BY SIMILARITY.
FT DISULFID 714 723 BY SIMILARITY.
FT DISULFID 730 741 BY SIMILARITY.
FT DISULFID 735 750 BY SIMILARITY.
FT DISULFID 752 761 BY SIMILARITY.
FT DISULFID 768 779 BY SIMILARITY.
FT DISULFID 773 788 BY SIMILARITY.
FT DISULFID 790 799 BY SIMILARITY.
FT DISULFID 807 818 BY SIMILARITY.
FT DISULFID 827 838 BY SIMILARITY.
FT DISULFID 845 856 BY SIMILARITY.
FT DISULFID 850 865 BY SIMILARITY.
FT DISULFID 867 876 BY SIMILARITY.
FT DISULFID 882 893 BY SIMILARITY.
FT DISULFID 897 912 BY SIMILARITY.

FT DISULFID 914 923 BY SIMILARITY.
FT DISULFID 930 941 BY SIMILARITY.
FT DISULFID 935 950 BY SIMILARITY.
FT DISULFID 952 961 BY SIMILARITY.
FT DISULFID 968 979 BY SIMILARITY.
FT DISULFID 973 988 BY SIMILARITY.
FT DISULFID 990 999 BY SIMILARITY.
FT DISULFID 1006 1019 BY SIMILARITY.
FT DISULFID 1011 1028 BY SIMILARITY.
FT DISULFID 1030 1039 BY SIMILARITY.
FT DISULFID 1046 1057 BY SIMILARITY.
FT DISULFID 1051 1069 BY SIMILARITY.
FT DISULFID 1071 1080 BY SIMILARITY.
FT DISULFID 1087 1098 BY SIMILARITY.
FT DISULFID 1092 1110 BY SIMILARITY.
FT DISULFID 1112 1121 BY SIMILARITY.
FT DISULFID 1130 1142 BY SIMILARITY.
FT DISULFID 1136 1155 BY SIMILARITY.
FT DISULFID 1157 1166 BY SIMILARITY.
FT CARBOHYD 711 711 POTENTIAL.
FT CARBOHYD 960 960 POTENTIAL.
FT CARBOHYD 1139 1139 POTENTIAL.
FT CONFLICT 43 43 Q -> R (IN REF. 3).
FT CONFLICT 298 298 L -> P (IN REF. 3).
.... remainder of annotations omitted.
Query Match 13.3%; Score 143; DB 1; Length 1964;
Best Local Similarity 32.6%; Pred. No. 8.65e-08;
Matches 43; Conservative 26; Mismatches 58; Indels 5; Gaps 5;
Db 1636 AARFSRPTAARLLLEAGANPNQDPBAGTPLHTVAADAREVCQQLLLASRQTSVDARTED 1695
QY 20 AAR-GRVEEVALLLEAVALPNAPNSYGRPIQVMMGSAAR-VAELLHLHGAEPNCADPAT 77
Db 1696 GTTPLMLAARLA-VEDLVEELIAARADYGDARKGKTALHWAAYNNARAARSL-LQAGA 1753
QY 78 LTRPVHDAAREGFLDTLVV-LHRAGARLDVRDANGRLPVDLAELGHRDVARLYLRAAAGG 136
Db 1754 DKDAQDSREQTP 1765
QY 137 TRGSNHARIDAA 148

Search completed: Thu Jul 20 08:35:53 2000
Job time : 10 secs.

MPSRELH

(TM)

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Mparch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:36:11 2000; Maspar time 18.43 Seconds
Tabular output not generated.
586.937 Million cell updates/sec

Title: >US-09-016-869A-2
Description: (1-156) from US09016869A.pep
Perfect Score: 1078
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 43.910; Variance 82.660; scale 0.531

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	749	69.5	115	4	Q16361 CELL CYCLE NEGATIVE RE	1.35e-131
2	678	62.9	168	11	P97510 CYCLIN DEPENDENT KINAS	3.53e-116
3	674	62.5	168	11	O89088 CYCLIN DEPENDENT KINAS	2.59e-115
4	621	57.6	102	6	P16/CDKN2A/MTS1 (FRAGM	7.07e-104
5	596	55.3	86	6	O9X552 P15/MTS2/CDKN2B (FRAGM	1.66e-98
6	566	52.5	86	11	O921C1 CYCLIN-DEPENDENT KINAS	4.38e-92
7	557	51.7	86	11	O54846 CYCLIN-DEPENDENT KINAS	3.66e-90
8	480	44.5	133	11	O921C2 CYCLIN-DEPENDENT KINAS	7.77e-74
9	379	35.2	124	13	P70067 CDKN2X PROTEIN.	8.17e-53
10	372	34.5	124	13	O9W618 P13CDKN2X.	2.22e-51
11	333	30.9	116	4	O95440 CYCLIN-DEPENDENT KINAS	1.89e-43
12	330	30.6	58	6	O97896 CYCLIN-DEPENDENT KINAS	7.63e-43
13	198	18.4	42	11	O921B8 P16INK4A TUMOR SUPPRES	2.67e-17
14	194	18.0	42	11	O921C3 CYCLIN-DEPENDENT KINAS	1.42e-16
15	177	16.4	843	11	P97582 ANKYRIN (FRAGMENT).	1.57e-13
16	174	16.1	1719	4	O13768 ALT. ANKYRIN (VARIANT)	5.32e-13
17	173	16.1	1856	4	O99407 ANKYRIN.	5.32e-13
18	173	16.0	1098	11	O61304 ANKYRIN 1, ERYTHROID (7.97e-13
19	173	16.0	1848	11	O61302 ANKYRIN 1, ERYTHROID (7.97e-13
20	170	15.8	1762	11	O88521 190 KDA ANKYRIN ISOFOR	2.67e-12

21	170	15.8	1943	11	O61307 ANKYRIN 3 (ANKYRIN G)	2.67e-12
22	170	15.8	2622	11	O70511 270 KDA ANKYRIN G ISO	2.67e-12
23	165	15.3	4377	4	ANKYRIN G.	1.97e-11
24	163	15.1	44	11	O921C0 CYCLIN-DEPENDENT KINAS	4.36e-11
25	162	15.0	1095	4	O99458 NOTCH4 (FRAGMENT).	6.48e-11
26	162	15.0	1999	4	O99940 NOTCH4.	6.48e-11
27	162	15.0	2003	4	O00306 NOTCH4.	6.48e-11
28	160	14.8	1435	5	O43997 K12C11.4 PROTEIN.	1.43e-10
29	160	14.8	1786	5	O17344 UNC-44 (FRAGMENT).	1.43e-10
30	160	14.8	1809	5	O17487 E. ELEGANS ANKYRIN-REL	1.43e-10
31	160	14.8	1815	5	O17488 C. ELEGANS ANKYRIN-REL	1.43e-10
32	160	14.8	1867	5	O17486 C. ELEGANS ANKYRIN-REL	1.43e-10
33	160	14.8	2039	5	O17489 C. ELEGANS ANKYRIN-REL	1.43e-10
34	160	14.8	6934	5	O17343 UNC-44 ANKYRINS.	1.43e-10
35	155	14.4	1088	4	O13484 ANKYRIN G119.	1.01e-09
36	153	14.2	78	4	O15125 ALTERNATIVE SPLICED FO	2.20e-09
37	152	14.1	1549	5	O24241 ANKYRIN.	3.24e-09
38	149	13.8	835	4	O9Y2V6 HYPOTHETICAL 92.9 KD P	1.03e-08
39	148	13.7	745	4	O9Y544 DJ20208.1 (NOVEL RAT E	1.51e-08
40	146	13.5	837	11	O63618 ESPIN.	3.24e-08
41	146	13.5	1327	4	O95271 TRF1-INTERACTING ANKYR	3.24e-08
42	142	13.2	554	11	O62390 SIMILAR TO MOUSE INT-3	1.47e-07
43	142	13.2	1964	11	O35442 NOTCH4.	1.47e-07
44	140	13.0	882	4	O15084 KIAA0379 (FRAGMENT).	3.13e-07
45	138	12.8	525	11	O9WV72 ANKYRIN REPEAT-CONTAIN	6.60e-07

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	115 AA.
ID Q16361			
AC Q16361			
DT 01-NOV-1996 (Tremblrel. 01, Created)			
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)			
DE CELL CYCLE NEGATIVE REGULATOR BETA FORM (FRAGMENT).			
GN P16/MTS1/CDKN2			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE; 95330726.			
RA STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H.,			
RA PARRY D., PETERS G., KAMB A.;			
RT "Complex structure and regulation of the P16 (MTS1) locus.";			
RL Cancer Res. 55:2988-2994(1995).			
DR EMBL; S78535; AAC60650.1; -.			
DR HSSP; P42771; 1BI7.			
FT NON_TER			
SQ SEQUENCE 115 AA; 12334 MW; F5BEF54B CRC32;			
Query Match	69.5%	Score 749;	DB 4; Length 115;
Best Local Similarity	100.0%	Pred. No. 1.35e-131;	
Matches	107;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db 9 QVMMGSRVAEELLHGAEPNCADPATLRPVHDAAREGFLDTLVVLRAGARLDVRDA 68			
QY 50 QVMMGSRVAEELLHGAEPNCADPATLRPVHDAAREGFLDTLVVLRAGARLDVRDA 109			
Db 69 WGRLPVDAEELGHRDVARVYLRAGRGSHARIDAAEGPSDIPD 115			
QY 110 WGRLPVDAEELGHRDVARVYLRAGRGSHARIDAAEGPSDIPD 156			
RESULT 2	PRELIMINARY;	PRT;	168 AA.
ID P97510			
AC P97510; P97937;			
DT 01-MAY-1997 (Tremblrel. 03, Created)			
DT 01-NOV-1999 (Tremblrel. 10, Last sequence update)			
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)			
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR			
DE PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16, INHIBITS CDK4)			


```
QY      111 GRLPVDLAEELGHDRVARYLRAAG 135

RESULT        6
ID   Q9Z1C1    PRELIMINARY;          PRT;         86 AA.
AC   Q9Z1C1
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN   p15.
OS   Mus spretus (Western wild mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RC   STRAIN=SPRETJEL;
RA   SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA   PELLICER A., FERNANDEZ-PIQUERAS J.;
RT   "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RL   in mouse inbred strains.";
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U75637; AAD00237.1; -.
DR   HSSP; P42771; IBI7.
KW   Kinase; Cyclin.
FT   NON_TER            1
FT   NON_TER            86
SQ   SEQUENCE      86 AA;  9269 MW;  D5811BE2 CRC32;

Query Match           52.5%; Score 566; DB 11; Length 86;
Best Local Similarity 92.9%; Pred. No. 4.38e-92;
Matches              79; Conservative       4; Mismatches     2; Indels    0; Gaps    0

Db      1 VMMSGSAQVAELLHGAEPCNCPATLTRPVHDAAREGFDLTIVLHRAGARLDVCDAW 60
QY      51 VMMSGSAQVAELLHGAEPCNCPATLTRPVHDAAREGFDLTIVLHRAGARLDVCDAW 110
               |||||
Db      61 GRLPVDLAEEOGHRDIARYLHAATG 85
               |||||
QY      111 GRLPVDLAEELGHDRVARYLRAAG 135
               |||||

RESULT        7
ID   O54846    PRELIMINARY;          PRT;         86 AA.
AC   O54846;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN   CDKN2B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RC   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RA   MALUMBRES M., PELLICER A.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF015460; AAB94534.1; -.
DR   HSSP; P42771; IBI7.
FT   NON_TER            1
FT   NON_TER            86
SQ   SEQUENCE      86 AA;  9237 MW;  FEC97F63 CRC32;

Query Match           51.7%; Score 557; DB 11; Length 86;
Best Local Similarity 91.8%; Pred. No. 3.66e-50;
Matches              78; Conservative       5; Mismatches     2; Indels    0; Gaps    0

Db      1 VMMSGSAQVAELLHGAEPCNCPATLTRPVHDAAREGFDLTIVLHRAGARLDVCDAW 60
QY      51 VMMSGSAQVAELLHGAEPCNCPATLTRPVHDAAREGFDLTIVLHRAGARLDVCDAW 110
               |||||
Db      61 GRLPVDLAEEOGHRDIARYLHAASG 85
               |||||
```



```
Db 1 MEPAAGSMPSADWLATAAARGVEVFRALLEAGALPNAPNSYGRPIQVGRRSARAG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MDPAGSSMPSADWLATAAARGVEVFRALLEAGALPNAPNSYGRPIQVMMMSARVA 60
61 D 61
61 E 61

RESULT 12
ID O97886 PRELIMINARY; PRT; 58 AA.
AC O97886;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).
GN CDKN2A.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKIN;
RA RIEDER S., CHECA-CORTES M.L., JOERG H., STRANZINGER G.;
RT "An equine sequence homologous to cyclin-dependent kinase inhibitor
(CDKN2A).";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076782; AAC97110.1; -.
DR HSSP; P42771; 1B17.
KW Kinase; Cyclin.
FT NON_TER 1
FT NON_TER 58
FT NON_TER 58
SQ SEQUENCE 58 AA; 6162 MW; DE8139C2 CRC32;

Query Match 30.6%; Score 330; DB 6; Length 58;
Best Local Similarity 83.3%; Pred. No. 7.63e-43; Indels 0; Gaps 0;
Matches 45; Conservative 5; Mismatches 4;

Db 5 PNGVNGFGRPIQVMMGSRVHVAELLHGGADPNRDPDTLRPVHDAAREGFL 58
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 38 PNAPNSYGRPIQVMMGSRVHVAELLHGGADPNRDPDTLRPVHDAAREGFL 91

RESULT 13
ID O92188 PRELIMINARY; PRT; 42 AA.
AC O92188;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE PL6INK4A TUMOR SUPPRESSOR PROTEIN (FRAGMENT).
GN ELAPHA.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J, A/WY, AKR/J, SJL/J, SWR/J, ST/J, LP/J, LS/IBG, SM/J,
RC HS/IBG, B10;
RA HERZOG C.R., YOU M.;
RT "Polymorphisms and chromosomal mapping of the murine pl6INK4a tumor
suppressor gene.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U51567; AAD09455.1; -.
DR HSSP; Q60773; 1AP7.
KW Kinase; Cyclin.
FT NON_TER 42
FT NON_TER 42
SQ SEQUENCE 42 AA; 4402 MW; 3CA62F1F CRC32;

Query Match 18.4%; Score 198; DB 11; Length 42;
Best Local Similarity 71.4%; Pred. No. 2.67e-17;
Matches 30; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 1 MESAADRLARAAAGRVHVDVRLLEAGVSPKAPNSFGRTPIQ 42
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 9 MEPSADWLATAAARGVEVFRALLEAGVSPKAPNSYGRPIQ 50

RESULT 14
ID O921C3 PRELIMINARY; PRT; 42 AA.
AC O921C3;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN p16.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRET/EI;
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA PELLICER A., FERNANDEZ-PIQUERAS J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79629; AAD00235.1; -.
DR HSSP; Q60773; 1AP7.
KW Kinase; Cyclin.
FT NON_TER 42
FT NON_TER 42
SQ SEQUENCE 42 AA; 4416 MW; A405580F CRC32;

Query Match 18.0%; Score 194; DB 11; Length 42;
Best Local Similarity 69.0%; Pred. No. 1.42e-16;
Matches 29; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1 MESAADRLARAAAGRVHVDVRLLEAGVSPKAPNSFGRTPIQ 42
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 9 MEPSADWLATAAARGVEVFRALLEAGVSPKAPNSYGRPIQ 50

RESULT 15
ID P97582 PRELIMINARY; PRT; 843 AA.
AC P97582;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE ANKYRIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-BRAIN;
RA COSENTINO M.T., JONES O.T.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U65916; AAB47551.1; -.
DR HSSP; Q00421; 1AWC.
DR PFAM; PF00023; ank; 22.
FT NON_TER 1
FT NON_TER 843
FT NON_TER 843
SQ SEQUENCE 843 AA; 89982 MW; D89BDC46 CRC32;

Query Match 16.4%; Score 177; DB 11; Length 843;
Best Local Similarity 38.1%; Pred. No. 1.57e-13;
Matches 48; Conservative 19; Mismatches 54; Indels 5; Gaps 4;

Db 436 AARAGEVEVVRCLLRNGALVDARAREEQTPHIASRLGKTEIVQLLQHHMAHPDAATNG 495
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 20 AAR-GRVEVFRALLEAGVSPKAPNSYGRPIQVMMGSRVHVAELLHGGADPNRDPDTLRPVHDAAREGFL 77

Db 496 YT-PLHISAREGVQDVASVLEAGAAHSLATKKGFTPLRHYAAYKYSVDVAKLLQRRAAA 554
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 78 LTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVARYL--RAAAG 135

Db 555 DSAGKN 560
```

OY 136 CTRGSN 141

Search completed: Thu Jul 20 08:36:32 2000
Job time : 21 secs.

MPERCH_PP

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:38:10 2000; MasPar time 6.72 Seconds

Tabular output not generated. 483.073 Million cell updates/sec

Title: >US-09-016-869A-4
Description: (1-137) from US09016869A.pep
Perfect Score: 977
Sequence: 1 MREENKGMPSGGSGDEGLAT.....LAERGHDRVAGYLTATGTD 137

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseq36
l:geneseqp

Statistics: Mean 30.377; Variance 133.757; scale 0.227

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	919	94.1	138	1	R80948 Human multiple tumour	3.58e-75
2	919	94.1	138	1	R81702 Multiple tumour suppressor	3.58e-75
3	919	94.1	138	1	W74553 Amino acid sequence 2	3.58e-75
4	919	94.1	138	1	W80526 A human multiple tumour	3.58e-75
5	919	94.1	138	1	W19255 Human multiple tumour	3.58e-75
6	919	94.1	138	1	W40526 Human MTS2 protein.	3.58e-75
7	907	92.8	138	1	R85117 Cell-cycle regulatory	5.05e-74
8	819	83.8	138	1	R85118 Cell-cycle regulatory	1.33e-65
9	757	77.5	130	1	R85119 Cell-cycle regulatory	1.09e-59
10	749	76.7	130	1	W70823 Mouse multiple tumour	6.31e-59
11	692	70.8	156	1	W19251 Human multiple tumour	1.66e-53
12	692	70.8	156	1	W80524 A human multiple tumour	1.66e-53
13	692	70.8	156	1	W10627 Tumour suppressor p16.	1.66e-53
14	692	70.8	156	1	W74549 Amino acid sequence of	1.66e-53
15	692	70.8	156	1	W40524 Human MTS1 protein.	1.66e-53
16	692	70.8	237	1	W95105 Truncated p27/p16 fusi	1.66e-53
17	692	70.8	252	1	W95103 Truncated p27/p16 fusi	1.66e-53
18	692	70.8	334	1	W95106 Human p16p27 fusion pr	1.66e-53
19	692	70.8	365	1	W95096 Human p16p27 fusion pr	1.66e-53
20	692	70.8	365	1	W95107 Human p16p27 fusion pr	1.66e-53
21	692	70.8	365	1	W23536 CDK inhibitory fusion	1.66e-53
22	692	70.8	380	1	W95095 Human p16(GS)p27 fusio	1.66e-53
23	692	70.8	380	1	W23535 CDK inhibitory fusion	1.66e-53

Multiple tumour suppressor 1.48e-52
Human multiple tumour 1.48e-52
Inhibitor of cyclin de 1.48e-52
Cell-cycle regulatory 1.48e-52
Human p27-p16 fusion p 1.48e-52
CDK inhibitory fusion p 1.48e-52
Human multiple tumour 1.84e-52
Human multiple tumour 6.82e-52
Truncated p27/p16 fusi 1.31e-51
Amino acid sequence 1 3.73e-42
Multiple tumour suppressor 3.73e-42
A human multiple tumour 3.73e-42
Human MTS1E1-beta prot 3.73e-42
Human multiple tumour 3.73e-42
Human multiple tumour 3.73e-42
Mouse multiple tumour 3.73e-42
Cell-cycle regulatory 1.20e-40
Human INK4a-p16 C-term 6.71e-34
Murine INK4a-p16 C-term 8.85e-33
Cell-cycle regulatory 2.33e-30
Cell-cycle regulatory 2.33e-30

ALIGNMENTS

RESULT 1
ID R80948 standard; Protein; 138 AA.

AC R80948;
DC 03-MAY-1996 (first entry)
DE Human multiple tumour suppressor polypeptide, MTS2.
KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
OS gene therapy; chronic.
OS Homo sapiens.
PD WO9525429-A1.
PN 28-SEP-1995.
PF 17-MAR-1995; U03315.
PR 18-MAR-1994; US-214581.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215088.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI: 95-344401/44.
DR N-PSDB: Q99165.
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
PT melanoma or leukaemia
PS Claim 5; Page 103; 156pp; English.
CC Several multiple tumour suppressor (MTS) polypeptides have been
CC isolated and sequenced. This sequence is the MTS polypeptide MTS2.
CC MTS polypeptide-encoding cDNAs and mutants of these are useful for
CC the diagnosis or prognosis of human cancer. Germ-line mutations of
CC MTS cDNAs can be used for diagnosing predisposition to melanoma,
CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's
CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,
CC testis, kidney, stomach and rectum. The wild-type gene is useful
CC for gene therapy and MTS polypeptides may also be used for protein
CC replacement therapy. Also the polypeptides or cells contg. an
CC altered MTS gene are useful for screening for potential cancer
CC therapeutics.
SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;

Best Local Similarity 95.7%; Pred. No. 3.58e-75;

Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

DB 1 MREENKGMPSGGSGDEGLASAAARGVLEKVRQLLEAGADPNGVNFRFRRRAIQVNMGSAR 60
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QY 1 MREENKMPGGGSGDEGLATPA-RGLVEKVRHSWEAGADPNCVNRFGRRRAIQVMMGSGAR 59
Db 61 VAEILLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLHHRAGARLDVRDAGRLPVDLA 120
QY 60 VAEILLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLHHRAGARLDVRDAGRLPVDLA 119
Db 121 EERGRDVGAGYLRTATGD 138
QY 120 EERGRDVGAGYLRTATGD 137

RESULT 2
ID R81702 standard; Protein; 138 AA.
AC R81702;
DE 08-MAY-1996 (first entry)
DE Multiple tumour suppressor 2 (MTS2) polypeptide.
KW Multiple tumour suppressor; MTS2; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid.
OS Homo sapiens.
PN W09525813-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR N-PSDB; T00745.
DR WPI; 95-344626/44.
DR N-PSDB; T00745.
PT Detecting polymorphism associated with cancer predisposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
PS Disclosure: Page 103; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to the MTS2
CC gene ORF T00745 (which encodes R81702). The above assay can also be
CC used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia
CC and pancreas, breast and thyroid cancers, etc.
SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPGGGSGDEGLASAAARGLVKVRQLLEAGADPNCVNRFGRRRAIQVMMGSGAR 60
QY 1 MREENKMPGGGSGDEGLATPA-RGLVEKVRHSWEAGADPNCVNRFGRRRAIQVMMGSGAR 59
Db 61 VAEILLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLHHRAGARLDVRDAGRLPVDLA 120
QY 60 VAEILLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLHHRAGARLDVRDAGRLPVDLA 119
Db 121 EERGRDVGAGYLRTATGD 138
QY 120 EERGRDVGAGYLRTATGD 137

RESULT 3
ID W74553 standard; Protein; 138 AA.
AC W74553;
DE 04-DEC-1998 (first entry)
DE Amino acid sequence 2 of the multiple tumour suppressor MTS1E1S.
KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;
KW somatic mutation; gene therapy.
OS Homo sapiens.
PN US5801236-A.
PD 01-SEP-1998.
PF 07-JUN-1995; 480810.

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PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-U03316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI; 98-494842/42.
DR N-PSDB; V53831.
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Disclosure: Fig 11; 73pp; English.
CC This is the amino acid sequence of the multiple tumour suppressor
CC (MTS1E1S) protein, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPGGGSGDEGLASAAARGLVKVRQLLEAGADPNCVNRFGRRRAIQVMMGSGAR 60
QY 1 MREENKMPGGGSGDEGLATPA-RGLVEKVRHSWEAGADPNCVNRFGRRRAIQVMMGSGAR 59
Db 61 VAEILLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLHHRAGARLDVRDAGRLPVDLA 120
QY 60 VAEILLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLHHRAGARLDVRDAGRLPVDLA 119
Db 121 EERGRDVGAGYLRTATGD 138
QY 120 EERGRDVGAGYLRTATGD 137

RESULT 4
ID W80526 standard; Protein; 138 AA.
AC W80526;
DE 03-FEB-1999 (first entry)
DE A human multiple tumour suppressor 2 (MTS2) protein.
KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
OS Homo sapiens.
PN US5843756-A.
PD 01-DEC-1998.
PF 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI; 99-044585/04.
DR N-PSDB; V70595.
PT Mouse multiple tumour suppressor gene segment - useful for primer
PT design
PS Example 6; Fig 11; 80pp; English.
CC The present sequence represents a human multiple tumour suppressor 2
CC (MTS2) protein. The sequence is homologous to the corresponding
CC murine gene. Primers designed from the gene can be used to design
CC primers to detect abnormalities i.e. polymorphisms which may
CC predispose towards malignancies such as melanoma, leukaemia,
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.

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SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPSSGGSGDEGLASAAAGLVKRYQLLEAGADPNVNRFRGRRRAIQVMMGSGAR 60
QY 1 MREENKMPSSGGSGDEGLATPA-RGLVEKYRHSWEAGADPNVNRFRGRRRAIQVMMGSGAR 59

Db 61 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
QY 60 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 119

Db 121 EERGRDVGAYLRTATGD 138
QY 120 EERGRDVGAYLRTATGD 137

RESULT 5
ID W19255 standard; Protein; 138 AA.
AC W19255;
DE 10-SEP-1997 (first entry)
KW Human multiple tumour suppressor 2 gene product.
OS Homo sapiens.
PN U55624819-A.
PD 29-APR-1997.
PF 18-MAR-1994; 214582.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003537.
PR 07-JUN-1995; US-474177.
PA (MYRI-) MYRIAD GENETICS INC.
PI (UTAH) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Ramb A, Skolnick MH;
DR WPI; 97-258217/23.
DR N-PSDB; T69781.
PT Human mutant multiple tumour suppressor gene sequences - for
PT production of recombinant mutant polypeptide(s)
PS Disclosure; Columns 73-74; 72pp; English.
CC The present sequence the human multiple tumour suppressor 2
CC (MTS2) gene product, useful in cancer diagnosis.
SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPSSGGSGDEGLASAAAGLVKRYQLLEAGADPNVNRFRGRRRAIQVMMGSGAR 60
QY 1 MREENKMPSSGGSGDEGLATPA-RGLVEKYRHSWEAGADPNVNRFRGRRRAIQVMMGSGAR 59

Db 61 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
QY 60 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 119

Db 121 EERGRDVGAYLRTATGD 138
QY 120 EERGRDVGAYLRTATGD 137

RESULT 6
ID W40526 standard; Protein; 138 AA.
AC W40526;
DE 13-JUL-1998 (first entry)
KW Human MTS2 protein.
DE Human MTS2; multiple tumour suppressor; diagnosis; cancer;
KW germ-line mutation; familial melanoma locus; MLM; predisposition.
OS Homo sapiens.

PN US5739027-A.
PD 14-APR-1998.
PF 07-JUN-1995; 487033.
PR 07-JUN-1995; US-487033.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Ramb A;
PI WPI; 98-250421/22.
DR N-PSDB; V11250.
PT DNA specific for Multiple Tumour Suppressor 1el-beta gene - are
PT useful for the diagnosis of cancers related to MTS1el-beta
PT mutation(s) and their treatment
PS Disclosure; Fig 11; 72pp; English.
CC This sequence represents a human multiple tumour suppression protein,
CC (MTS2). The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.
SQ Sequence 138 AA;

Query Match 94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 3.58e-75;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPSSGGSGDEGLASAAAGLVKRYQLLEAGADPNVNRFRGRRRAIQVMMGSGAR 60
QY 1 MREENKMPSSGGSGDEGLATPA-RGLVEKYRHSWEAGADPNVNRFRGRRRAIQVMMGSGAR 59

Db 61 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
QY 60 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 119

Db 121 EERGRDVGAYLRTATGD 138
QY 120 EERGRDVGAYLRTATGD 137

RESULT 7
ID R85117 standard; Protein; 138 AA.
AC R85117;
DE 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein p15.
KW Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
KW CCR; cancer; cell proliferation.
OS Homo sapiens.
PN WO9528483-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04636.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
DR WPI; 95-373798/48.
DR N-PSDB; T02963.
PT New cell cycle regulating proteins bind to cyclin dependent kinase -
PT and related nucleic acids, antibodies etc., used in diagnosis and
PT therapy of abnormal cell proliferation, degeneration etc.
PS Claim 8; Page 78; 109pp; English.
CC The human cell-cycle regulatory (CCR) protein p15 (R85117) was
CC obt'd. by expression of a cDNA clone (T02963) isolated from
CC transforming growth factor-stimulated Hecar cells. CCR p15
CC specifically inhibits the activity of cyclin-dependent kinases
CC during various stages of the cell cycle, and can be used in the
CC treatment and diagnosis of proliferative disorders.

SQ Sequence 138 AA;
 Query Match 92.8%; Score 907; DB 1; Length 138;
 Best Local Similarity 94.9%; Pred. No. 5.05e-74;
 Matches 131; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 Db 1 MREENKMPSGGSGDEGLASAAARGLVEKVRQLLEAGADPNVFRGRRRAIQVMMGSGAR 60
 QY 1 MREENKMPSGGSGDEGLATPA-RGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGAR 59
 Db 61 VAEILLHGAENPCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLA 120
 QY 60 VAEILLHGAENPCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLA 119
 Db 121 EERGRDVAGYLRTATGD 138
 QY 120 EERGRDVAGYLRTATGD 137
 RESULT 8
 ID R85115 standard; Protein; 138 AA.
 AC R85115;
 DT 01-MAR-1996 (first entry)
 DE Cell-cycle regulatory protein p15 homologue.
 KW Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
 KW CCR; cell proliferation; agonist; antagonist.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_difference 57. .59
 FT /note= "unidentified amino acids"
 FT misc_difference 62
 FT /note= "unidentified amino acid"
 FT misc_difference 66. .67
 FT /note= "unidentified amino acids"
 FT misc_difference 70. .71
 FT /note= "unidentified amino acids"
 FT misc_difference 74
 FT /note= "unidentified amino acid"
 FT misc_difference 77
 FT /note= "unidentified amino acid"
 FT misc_difference 79. .81
 FT /note= "unidentified amino acid"
 FT misc_difference 101. 102
 FT /note= "unidentified amino acids"
 FT misc_difference 117
 FT /note= "unidentified amino acid"
 FT misc_difference 121
 FT /note= "unidentified amino acid"
 FT misc_difference 123
 FT /note= "unidentified amino acid"
 FT misc_difference 126
 FT /note= "unidentified amino acid"
 FT misc_difference 128. .130
 FT /note= "unidentified amino acids"
 FT misc_difference 134
 FT /note= "unidentified amino acid"
 FT misc_difference 136
 FT /note= "unidentified amino acid"
 PN W09528483-A1.
 PD 26-OCT-1995.
 PF 14-APR-1995; U04636.
 PR 14-APR-1994; US-227371.
 PR 25-MAY-1994; US-248812.
 PR 14-SEP-1994; US-306511.
 PR 29-NOV-1994; US-346147.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
 DR WPI; 95-373798/48.
 PT New cell cycle regulating proteins bind to cyclin dependent kinase -
 PT and related nucleic acids, antibodies etc., used in diagnosis and
 PT therapy of abnormal cell proliferation, degeneration etc.
 PS Claim 16; Page 87-88; 109pp; English.
 CC A homologue (R85115) of the human cell-cycle regulatory (CCR) protein

CC p15, showing at least 60% homology to p15 (R85117), functions as either
 CC an agonist or antagonist of cell cycle regulation.
 SQ Sequence 138 AA;
 Query Match 83.8%; Score 819; DB 1; Length 138;
 Best Local Similarity 82.6%; Pred. No. 1.33e-65;
 Matches 114; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
 Db 1 MREENKMPSGGSGDEGLATPARGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGARV 60
 QY 1 MREENKMPSGGSGDEGLATPARGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGARV 60
 Db 61 AXLLXXGAXXNCXDPXTXXRPHVDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLA 120
 QY 61 AELLLLHGAENPCADPATLT-RPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLA 119
 Db 121 XEXGHDXXXYLXAXGD 138
 QY 120 EERGRDVAGYLRTATGD 137
 RESULT 9
 ID R85118 standard; Protein; 130 AA.
 AC R85118;
 DT 01-MAR-1996 (first entry)
 DE Cell-cycle regulatory protein p15.
 KW Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
 KW CCR; cancer; cell proliferation.
 OS Mus sp.
 PN W09528483-A1.
 PD 26-OCT-1995.
 PF 14-APR-1995; U04636.
 PR 14-APR-1994; US-227371.
 PR 25-MAY-1994; US-248812.
 PR 14-SEP-1994; US-306511.
 PR 29-NOV-1994; US-346147.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
 DR WPI; 95-373798/48.
 PT New cell cycle regulating proteins bind to cyclin dependent kinase -
 PT and related nucleic acids, antibodies etc., used in diagnosis and
 PT therapy of abnormal cell proliferation, degeneration etc.
 PS Claim 9; Page 81-82; 109pp; English.
 CC The mouse cell-cycle regulatory (CCR) protein p15 (R85118) was
 CC obtd. by expression of a cDNA clone (T02964) isolated from
 CC mouse embryonal carcinoma cells. CCR p15 specifically inhibits the
 CC activity of cyclin-dependent kinases during various stages of the
 CC cell cycle, and can be used in the treatment and diagnosis of
 CC proliferative disorders.
 SQ Sequence 130 AA;
 Query Match 77.5%; Score 757; DB 1; Length 130;
 Best Local Similarity 85.9%; Pred. No. 1.09e-59;
 Matches 110; Conservative 10; Mismatches 7; Indels 1; Gaps 1;
 Db 3 GGSSDAGLATAAARGQVETVQLLEAGADPNALNFRGRRRAIQVMMGSGARVAELLHGA 62
 QY 11 GGGSDAGLATPA-RGLVEKVRHSWEAGADPNVFRGRRRAIQVMMGSGARVAELLHGA 69
 Db 63 EPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAEEQGRDAR 122
 QY 70 EPNCADPATLTPVPHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAEEGRDVAR 129
 Db 123 YLHAATGD 130
 QY 130 YLRTATGD 137
 RESULT 10
 ID W70823 standard; Protein; 130 AA.
 AC W70823;
 DT 03-FEB-1999 (first entry)

DE Mouse multiple tumour suppressor 2 (MTS2) protein.
 KW Murine; multiple tumour suppressor 2 gene; MTS2; cancer.
 OS Mus musculus.
 PN 01-DEC-1998. 058735.
 PD 28-JUL-1995; US-508735.
 PR 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI: 99-044585/04.
 DR N-PSDB: V70624.
 PT Mouse multiple tumour suppressor gene segment - useful for primer design.
 PT Example 7; Fig 19; 80pp; English.
 PS The present sequence represents mouse multiple tumour suppressor 2 (MTS2) gene. The MTS1 gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose CC towards malignancies such as melanoma, leukaemia, astrocytoma, CC lymphoma, glioma, as well as tumours of e.g. the breast, CC thyroid, pancreas, uterus and kidneys.
 SQ Sequence 130 AA;

Query Match 76.78; Score 749; DB 1; Length 130;
 Best Local Similarity 85.28; Pred. No. 6.31e-59;
 Matches 109; Conservative 11; Mismatches 7; Indels 1; Gaps 1;
 DB 3 GGSAGLATAAARGQVETVQLLEAGADPNALNRGRRPQVMMGSAQVAELLLHGA 62
 QY 11 GGSAGLATAAARGQVETVQLLEAGADPNALNRGRRPQVMMGSAQVAELLLHGA 69
 DB 63 EPCADPATITRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAEEGHRDIA 122
 QY 70 EPCADPATITRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAEEGHRDIA 129
 DB 123 YLHAATGD 130
 QY 130 YLHAATGD 137

RESULT 11
 ID W19251 standard; Protein; 156 AA.
 AC W19251;
 DT 10-SEP-1997 (first entry)
 DE Human multiple tumour suppressor 1 gene product.
 KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
 OS Homo sapiens.
 PN US5624819-A.
 PD 29-APR-1997.
 PF 18-MAR-1994; 214582.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-003537.
 PR 07-JUN-1995; US-474177.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI (UTAH) UNIV UTAH RES FOUND.
 PI Cannon-Albright LA, Kamb A, Skolnick MH;
 DR WPI: 97-258217/23.
 DR N-PSDB: T72311.
 PT Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s)
 PS Claim 1; Columns 61-64; 72pp; English.
 CC The present sequence the human multiple tumour suppressor 1 (MTS1) gene product, useful in cancer diagnosis.
 SQ Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;
 Best Local Similarity 85.8%; Pred. No. 1.66e-53;
 Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
 DB 16 LATAAARGVEEVRALLEAGALPNAPNSYGRRRPQVMMGSAQVAELLLHGAEPNCADP 75
 QY 18 LATPA-RGLVKYRHSWEAGADPNVRFRRRAIQVMMGSAQVAELLLHGAEPNCADP 76
 DB 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAEEGHRDVARYLRAAG 135
 QY 77 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAEEGHRDVARYLRTATG 136

RESULT 13
 ID W10627 standard; Protein; 156 AA.
 AC W10627;
 DT 28-OCT-1997 (first entry)
 DE Tumour suppressor p16.
 KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4; cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
 KW anti-angiogenic activity; hyperproliferative disorder.
 OS Homo sapiens.
 PN WO9703635-A2.
 PD 06-FEB-1997.
 PF 17-JUL-1996; U11787.
 PR 17-JUL-1995; US-502881.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Jin X, Roth J;
 DR WPI: 97-132336/12.
 DR N-PSDB: T60951.
 PT Expression construct contg. DNA for tumour suppressor p16 - to restore p16 activity to transformed cells, useful for treating lung or bladder cancer or melanoma
 PS Disclosure: Fig 1b; 92pp; English.
 CC This sequence represents the tumour suppressor p16. The DNA encoding this sequence is joined to a promoter functional in eukaryotic cells and

DB 16 LATAAARGVEEVRALLEAGALPNAPNSYGRRRPQVMMGSAQVAELLLHGAEPNCADP 75
 QY 18 LATPA-RGLVKYRHSWEAGADPNVRFRRRAIQVMMGSAQVAELLLHGAEPNCADP 76
 DB 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAEEGHRDVARYLRAAG 135
 QY 77 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAEEGHRDVARYLRTATG 136

RESULT 12
 ID W80524 standard; Protein; 156 AA.
 AC W80524;
 DT 03-FEB-1999 (first entry)
 DE A human multiple tumour suppressor 1 (MTS1) protein.
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
 OS Homo sapiens.
 PN US5843756-A.
 PD 01-DEC-1998.
 PF 28-JUL-1995; 058735.
 PR 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI: 99-044585/04.
 DR N-PSDB: V70583.
 PT Mouse multiple tumour suppressor gene segment - useful for primer design.
 PS Disclosure; Columns 65-66; 80pp; English.
 CC The present sequence represents a human multiple tumour suppressor 1 (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design CC primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, CC thyroid, pancreas, uterus and kidneys.
 SQ Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;
 Best Local Similarity 85.8%; Pred. No. 1.66e-53;
 Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
 DB 16 LATAAARGVEEVRALLEAGALPNAPNSYGRRRPQVMMGSAQVAELLLHGAEPNCADP 75
 QY 18 LATPA-RGLVKYRHSWEAGADPNVRFRRRAIQVMMGSAQVAELLLHGAEPNCADP 76
 DB 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAEEGHRDVARYLRAAG 135
 QY 77 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAEEGHRDVARYLRTATG 136

RESULT 13
 ID W10627 standard; Protein; 156 AA.
 AC W10627;
 DT 28-OCT-1997 (first entry)
 DE Tumour suppressor p16.
 KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4; cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
 KW anti-angiogenic activity; hyperproliferative disorder.
 OS Homo sapiens.
 PN WO9703635-A2.
 PD 06-FEB-1997.
 PF 17-JUL-1996; U11787.
 PR 17-JUL-1995; US-502881.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Jin X, Roth J;
 DR WPI: 97-132336/12.
 DR N-PSDB: T60951.
 PT Expression construct contg. DNA for tumour suppressor p16 - to restore p16 activity to transformed cells, useful for treating lung or bladder cancer or melanoma
 PS Disclosure: Fig 1b; 92pp; English.
 CC This sequence represents the tumour suppressor p16. The DNA encoding this sequence is joined to a promoter functional in eukaryotic cells and

used in the expression construct of the invention. p16 is an inhibitory subunit, which is involved in the control of cyclin-dependent kinase 4 activity, and functions as a tumour suppressor. By detecting this sequence or the DNA encoding it, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore p16 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inserted in the antisense orientation, the expression construct inhibits p16 function. Reduced or increased levels of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by Southern or Northern blot, antibody immunoblot, fluorescent cell sorting or immunoassay.

Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;
Best Local Similarity 85.8%; Pred. No. 1.66e-53;
Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEEVALLLEAGALPNAPNSYGRPPQVMMGSGARVAELLLHGAEPNCADP 75
Qy 18 LATPA-RGLVEKVRHSWEAGADPNVRFGRRAIQVMMGSGARVAELLLHGAEPNCADP 76
Db 76 ATLTPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRAAG 135
Qy 77 ATLTPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAERGRDVGAGYLRATG 136

RESULT 14

ID W74549 standard; Protein; 156 AA.

AC W74549;
DT 04-DEC-1998 (first entry)
DE Amino acid sequence of multiple tumour suppressor 1.
KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy.
OS Homo sapiens.
PN US5801236-A.

PD 01-SEP-1998.
PF 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-U03316.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 98-494842/43.

DR N-PSDB; V53819.

PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s).

PS Disclosure; Column 63-64; 73pp; English.

CC This is the amino acid sequence of the multiple tumour suppressor 1
CC (MTS-1) protein, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic acid hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.

Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;
Best Local Similarity 85.8%; Pred. No. 1.66e-53;
Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEEVALLLEAGALPNAPNSYGRPPQVMMGSGARVAELLLHGAEPNCADP 75
Qy 18 LATPA-RGLVEKVRHSWEAGADPNVRFGRRAIQVMMGSGARVAELLLHGAEPNCADP 76
Db 76 ATLTPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRAAG 135
Qy 77 ATLTPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAERGRDVGAGYLRATG 136

RESULT 15

ID W40524 standard; Protein; 156 AA.

AC W40524; 1998 (first entry)

DE Human MTS1 protein.

KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;

KW familial melanoma locus; MLM; predisposition.

OS Homo sapiens.

PN US5739027-A.

PD 14-APR-1998.

PF 07-JUN-1995; 487033.

PR 07-JUN-1995; US-487033.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PR 17-MAR-1995; WO-U03316.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 98-250421/22.

DR N-PSDB; V11238.

PT DNA specific for Multiple Tumour Suppressor 1el-beta gene - are

PT useful for the diagnosis of cancers related to MTS1el-beta

PT mutation(s) and their treatment

PS Disclosure; Column 63-64; 72pp; English.

CC This sequence represents a human multiple tumour suppression protein,
CC MTS1. The MTS gene locus is also referred to as the familial melanoma

CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,

CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,

CC ovary, uterus, testis, kidney, stomach and rectum.

CC Sequence 156 AA;

Query Match 70.8%; Score 692; DB 1; Length 156;

Best Local Similarity 85.8%; Pred. No. 1.66e-53;

Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEEVALLLEAGALPNAPNSYGRPPQVMMGSGARVAELLLHGAEPNCADP 75
Qy 18 LATPA-RGLVEKVRHSWEAGADPNVRFGRRAIQVMMGSGARVAELLLHGAEPNCADP 76
Db 76 ATLTPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAELGHRDVARYLRAAG 135
Qy 77 ATLTPVHDAAREGFLDTLVVLRHAGARLDVWDAGRLPVDLAERGRDVGAGYLRATG 136

Search completed: Thu Jul 20 08:38:18 2000

Job time : 8 secs.

MPSRELH
(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Jul 20 08:40:10 2000; MasPar time 5.21 Seconds
379.758 Million cell updates/sec
Tabular output not generated.

Title: >US-09-016-869A-4
Description: (1-137) from US09016869A.pep
Perfect Score: 977
Sequence: 1 MREENKMGPGSGGSGDEGLAT.....LAERGHDRVAGYLRTATGD 137

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 28.536; Variance 128.899; scale 0.221

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	977	100.0	137	2	US-08-306-Sequence 4, Applicatio	2.17e-79
2	977	100.0	137	2	US-08-893-Sequence 4, Applicatio	2.17e-79
3	959	98.2	136	4	PCT-US96-0 Sequence 6, Applicatio	1.06e-77
4	919	94.1	138	4	PCT-US95-0 Sequence 4, Applicatio	5.92e-74
5	919	94.1	138	3	US-09-120-Sequence 16, Applicati	5.92e-74
6	919	94.1	138	3	US-08-581-Sequence 4, Applicatio	5.92e-74
7	919	94.1	138	2	US-08-486-Sequence 16, Applicati	5.92e-74
8	919	94.1	138	2	US-08-508-Sequence 16, Applicati	5.92e-74
9	919	94.1	138	1	US-08-480-Sequence 16, Applicati	5.92e-74
10	919	94.1	138	3	US-08-384-Sequence 25, Applicati	5.92e-74
11	919	94.1	138	2	US-08-474-Sequence 16, Applicati	5.92e-74
12	919	94.1	138	2	US-08-627-Sequence 4, Applicatio	5.92e-74
13	919	94.1	138	2	US-08-848-Sequence 16, Applicati	5.92e-74
14	919	94.1	138	1	US-08-487-Sequence 16, Applicati	5.92e-74
15	819	83.8	138	3	PCT-US95-0 Sequence 13, Applicati	1.32e-64
16	757	77.5	130	4	PCT-US95-0 Sequence 8, Applicatio	7.98e-59
17	757	77.5	130	2	US-08-627-Sequence 8, Applicatio	7.98e-59
18	757	77.5	130	3	US-08-581-Sequence 8, Applicatio	7.98e-59
19	749	76.7	130	2	US-08-508-Sequence 47, Applicati	4.44e-58
20	692	70.8	156	1	US-08-480-Sequence 2, Applicatio	8.82e-53
21	692	70.8	156	1	US-08-474-Sequence 2, Applicatio	8.82e-53
22	692	70.8	156	1	US-08-487-Sequence 2, Applicatio	8.82e-53
23	692	70.8	156	3	US-09-120-Sequence 2, Applicatio	8.82e-53

24	692	70.8	156	2	US-08-508-Sequence 2, Applicatio	8.82e-53
25	692	70.8	156	2	US-08-486-Sequence 2, Applicatio	8.82e-53
26	692	70.8	156	2	US-08-848-Sequence 2, Applicatio	8.82e-53
27	682	69.8	148	4	PCT-US93-0 Sequence 4, Applicatio	7.48e-52
28	682	69.8	148	3	US-08-384-Sequence 16, Applicati	7.48e-52
29	682	69.8	148	3	US-08-384-Sequence 24, Applicati	7.48e-52
30	682	69.8	148	1	US-08-154-Sequence 4, Applicatio	7.48e-52
31	682	69.8	156	4	PCT-US95-0 Sequence 2, Applicatio	7.48e-52
32	682	69.8	156	2	US-08-627-Sequence 2, Applicatio	7.48e-52
33	682	69.8	156	3	US-08-581-Sequence 2, Applicatio	7.48e-52
34	682	69.8	156	2	US-08-893-Sequence 2, Applicatio	7.48e-52
35	682	69.8	156	2	US-08-306-Sequence 2, Applicatio	7.48e-52
36	682	69.8	321	1	US-08-589-Sequence 2, Applicatio	7.48e-52
37	671	68.7	157	4	PCT-US96-0 Sequence 5, Applicatio	7.83e-51
38	628	64.3	88	3	US-08-581-Sequence 38, Applicati	1.29e-43
39	593	60.7	89	3	US-08-581-Sequence 37, Applicati	1.29e-43
40	581	59.5	167	2	US-08-627-Sequence 6, Applicatio	1.65e-42
41	572	58.5	105	3	US-09-120-Sequence 14, Applicati	1.11e-41
42	572	58.5	105	2	US-08-486-Sequence 14, Applicati	1.11e-41
43	572	58.5	105	2	US-08-508-Sequence 14, Applicati	1.11e-41
44	572	58.5	105	1	US-08-474-Sequence 14, Applicati	1.11e-41
45	572	58.5	168	2	US-08-508-Sequence 46, Applicati	1.11e-41

ALIGNMENTS

RESULT 1
ID US-08-306-511A-4 STANDARD; PRT; 137 AA.
XX
AC
XX
XX
DT
XX
XX
Sequence 4, Application US/08306511A
Sequence 4, Application US/08306511A
Patent No. 5962316
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SQ SEQUENCE 137 AA; 14746 MW; 80670 CN;

Query Match 100.0%; Score 977; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.17e-79;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MREENKMPGGSGGDEGLATPARGLVEKVRHSWEAGADPNVNRFGRRATQVMMGSAV 60
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QY 1 MREENKMPGGSGGDEGLATPARGLVEKVRHSWEAGADPNVNRFGRRATQVMMGSAV 60
|||||
Db 61 AELLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
|||||
QY 61 AELLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
|||||

Db 121 ERGRDVGAYLRTATGD 137
|||||
QY 121 ERGRDVGAYLRTATGD 137
|||||

RESULT 2
ID US-08-893-274-4 STANDARD; PRT; 137 AA.
XX AC xxxxxx
XX DT
XX

Sequence 4, Application US/08893274

Sequence 4, Application US/08893274
Patent No. 5968821
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:

CC NAME: Vincent, Matthew P.
CC REGISTRATION NUMBER: 36,709
CC REFERENCE/DOCKET NUMBER: MIV-071.09
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 832-1000
CC TELEFAX: (617) 832-7000
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 137 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 137 AA; 14746 MW; 80670 CN;

Query Match 100.0%; Score 977; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.17e-79;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MREENKMPGGSGGDEGLATPARGLVEKVRHSWEAGADPNVNRFGRRATQVMMGSAV 60
|||||
QY 1 MREENKMPGGSGGDEGLATPARGLVEKVRHSWEAGADPNVNRFGRRATQVMMGSAV 60
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Db 61 AELLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
|||||
QY 61 AELLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
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Db 121 ERGRDVGAYLRTATGD 137
|||||
QY 121 ERGRDVGAYLRTATGD 137
|||||

RESULT 3
ID PCT-US96-05252-6 STANDARD; PRT; 136 AA.
XX AC xxxxxx
XX DT
XX

Sequence 6, Application PC/TUS9605252

Sequence 6, Application PC/TUS9605252
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: p19: A Cell Cycle Inhibitor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05252
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 02307B-059910PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

CC LENGTH: 136 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..136
CC OTHER INFORMATION: /note= "human p15"
SQ SEQUENCE 136 AA; 14689 MW; 79498 CN;

Query Match 98.2%; Score 959; DB 4; Length 136;
Best Local Similarity 99.3%; Pred. No. 1.06e-77;
Matches 136; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 MREENKMGPSGGSGDE-LATPARGLVKVRHSWEAGADPNGVNRFGRRRAIQVMMGSGARV 59
QY 1 MREENKMGPSGGSGDEGLATPARGLVKVRHSWEAGADPNGVNRFGRRRAIQVMMGSGARV 60
Db 60 AELLLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAE 119
QY 61 AELLLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAE 120
Db 120 ERGRDVGAGYLRTATGD 136
QY 121 ERGRDVGAGYLRTATGD 137

RESULT 4
ID PCT-US95-04636-4 STANDARD; PRT; 138 AA.
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AC xxxxxx
XX
DT
XX
DE
XX
CC Sequence 4, Application PC/TUS9504636
CC Sequence 4, Application PC/TUS9504636
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
CC NUMBER OF SEQUENCES: 10
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Ascii(text)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04636
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/346,147
CC FILING DATE: 29-NOV-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/306,511
CC FILING DATE: 14-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/248,812
CC FILING DATE: 25-MAY-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,371
CC FILING DATE: 14-APR-1994
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;

Query Match 94.1%; Score 919; DB 4; Length 138;

Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMGPSGGSGDEGLASAAARGLVKVRQLLEAGADPNGVNRFGRRRAIQVMMGSGAR 60
QY 1 MREENKMGPSGGSGDEGLATPA-RGLVEKVRHSWEAGADPNGVNRFGRRRAIQVMMGSGAR 59
Db 61 VAELLLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLA 120
QY 60 VAELLLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLA 119
Db 121 ERGRDVGAGYLRTATGD 138
QY 120 ERGRDVGAGYLRTATGD 137

RESULT 5
ID US-09-120-130-16 STANDARD; PRT; 138 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
CC Sequence 16, Application US/09120130
CC Sequence 16, Application US/09120130
CC Patent No. 6037462
CC GENERAL INFORMATION:
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS1 GENE
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/120,130
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/480,810
CC FILING DATE:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:

CC PRIOR APPLICATION DATA: US 08/251,938
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 01-JUN-1994
CC PRIOR APPLICATION DATA: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA: US 08/215,086
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC PRIOR APPLICATION DATA: US 08/227,369
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA: US 08/214,582
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348-B
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;

Query Match 94.1%; Score 919; DB 2; Length 138;
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPGGSGGDEGLASAAAGLVKVRQLLEAGADPNGVNFRGRRATQVNMVMSAR 60
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Db 61 VAEILLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVDRAGRLPVDLA 120
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QY 120 EERGRDVGAYLRTATGD 137

RESULT 8
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XX
AC xxxxxx
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DT
XX
DE
XX
Sequence 16, Application US/08508735
Sequence 16, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
CC APPLICANT: Stone, Steven
CC APPLICANT: Jiang, Ping
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
CC NUMBER OF SEQUENCES: 47
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM: Floppy disk
CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/508,735
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US to be assigned
CC FILING DATE: 07-JUN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/03316
CC FILING DATE: 17-MAR-1995
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4848
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;

Query Match 94.1%; Score 919; DB 2; Length 138;
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Db 1 MREENKMPGGSGGDEGLASAAAGLVKVRQLLEAGADPNGVNFRGRRATQVNMVMSAR 60
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Sequence 16, Application US/08480810
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Patent No. 5801236
GENERAL INFORMATION:
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS1 GENE
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM: Floppy disk
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CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
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CC MEDIUM TYPE: Floppy disk
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 CC SOFTWARE: Patent Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/474,177
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/03537
 CC FILING DATE: 17-MAR-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/251,938
 CC FILING DATE: 01-JUN-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/215,087
 CC FILING DATE: 18-MAR-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/215,086
 CC FILING DATE: 18-MAR-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/227,369
 CC FILING DATE: 14-APR-1994
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/214,582
 CC FILING DATE: 18-MAR-1994
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Ihnen, Jeffrey L.
 CC REGISTRATION NUMBER: 28,957
 CC REFERENCE/DOCKET NUMBER: 24884-109348-E
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 202-962-4810
 CC TELEFAX: 202-962-8300
 CC INFORMATION FOR SEQ ID NO: 16:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 138 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 138 AA; 14722 MW; 80871 CN;
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 CC Query Match 94.1%; Score 919; DB 1; Length 138;
 CC Best Local Similarity 95.7%; Pred. No. 5.92e-74;
 CC Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
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 QY 60 VAEILLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLA 119
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 QY 120 EERGHDRVAGYLRTATGD 137
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 CC ID US-08-627-610-4 STANDARD; PRT; 138 AA.
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 CC DT
 CC DE
 CC Sequence 4, Application US/08627610
 CC Sequence 4, Application US/08627610
 CC Patent No. 5919997
 CC GENERAL INFORMATION:
 CC APPLICANT: Beach, David H.
 CC APPLICANT: Serrano, Manuel
 CC APPLICANT: Depinho, Ronald A.

CC TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
 CC TITLE OF INVENTION: Regulation
 CC NUMBER OF SEQUENCES: 13
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: LAHIVE & COCKFIELD
 CC STREET: 60 State Street
 CC CITY: Boston
 CC STATE: MA
 CC COUNTRY: USA
 CC ZIP: 02109
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
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 CC SOFTWARE: ASCII(text)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/627,610
 CC FILING DATE: 04-APR-1996
 CC CLASSIFICATION: 800
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Vincent, Matthew P.
 CC REGISTRATION NUMBER: 36,709
 CC REFERENCE/DOCKET NUMBER: CSI-001CP6
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (617) 227-7400
 CC TELEFAX: (617) 227-5941
 CC INFORMATION FOR SEQ ID NO: 4:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 138 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 138 AA; 14722 MW; 80871 CN;
 CC
 CC Query Match 94.1%; Score 919; DB 2; Length 138;
 CC Best Local Similarity 95.7%; Pred. No. 5.92e-74;
 CC Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
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 Db 1 MREENKMGPSGGSGDEGLASAAAGLVKRVKRLLEAGADPNGVNRFRGRRRAIQVMMGSGAR 60
 QY 1 MREENKMGPSGGSGDEGLATPA-RGLVKRVHSWEAGADPNGVNRFRGRRRAIQVMMGSGAR 59
 Db 61 VAEILLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLA 120
 QY 60 VAEILLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLA 119
 Db 121 EERGHDRVAGYLRTATGD 138
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 CC ID US-08-848-251-16 STANDARD; PRT; 138 AA.
 CC AC xxxxxx
 CC XX
 CC DT
 CC DE
 CC Sequence 16, Application US/08848251
 CC Sequence 16, Application US/08848251
 CC Patent No. 5989815
 CC GENERAL INFORMATION:
 CC APPLICANT: Skolnick, Mark H.
 CC APPLICANT: Cannon-Albright, Lisa A.
 CC APPLICANT: Kamb, Alexander
 CC TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
 CC TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MT
 CC NUMBER OF SEQUENCES: 36
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 CC STREET: 1201 New York Avenue, Suite 1000

CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/848,251
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/474,083
CC FILING DATE: 07-JUN-1995
CC APPLICATION NUMBER: PCT/US95/03537
CC FILING DATE: 17-MAR-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
CC APPLICATION DATA:
CC APPLICATION NUMBER: US 08/215,087
CC FILING DATE: 18-MAR-1994
CC APPLICATION NUMBER: US 08/215,086
CC FILING DATE: 18-MAR-1994
CC APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,369
CC FILING DATE: 14-APR-1994
CC APPLICATION DATA:
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348-G
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;

Query Match 94.1%; Score 919; DB 2; Length 138;
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Db 1 MREENKMGPSGGSGDEGLASAAAGLVKVRQLLEAGADPNVNRFGRRRAIQVMMGSGAR 60
QY 1 MREENKMGPSGGSGDEGLATPA-RGLVEKVRHSEWAGADPNVNRFGRRRAIQVMMGSGAR 59
Db 61 VAEILLHGAEPNCADPATLTFRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLA 120
QY 60 VAEILLHGAEPNCADPATLTFRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLA 119
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QY 120 EERGHDRVAGYLRTATGD 137

RESULT 14
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Sequence 16, Application US/08487033

XX Sequence 16, Application US/08487033
CC Patent No. 5739027
CC GENERAL INFORMATION:
CC APPLICANT: Kamb, Alexander
CC TITLE OF INVENTION: MTS1E1-Beta GENE
CC NUMBER OF SEQUENCES: 36
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
CC STREET: 1201 New York Avenue, Suite 1000
CC CITY: Washington
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
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CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
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CC APPLICATION NUMBER: PCT/US95/03316
CC FILING DATE: 17-MAR-1995
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CC APPLICATION NUMBER: US 08/251,938
CC FILING DATE: 01-JUN-1994
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CC FILING DATE: 18-MAR-1994
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CC FILING DATE: 18-MAR-1994
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CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/214,582
CC FILING DATE: 18-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ihnen, Jeffrey L.
CC REGISTRATION NUMBER: 28,957
CC REFERENCE/DOCKET NUMBER: 24884-109348-C
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-962-4810
CC TELEFAX: 202-962-8300
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 138 AA; 14722 MW; 80871 CN;
Query Match 94.1%; Score 919; DB 1; Length 138;
Best Local Similarity 95.7%; Pred. No. 5.92e-74;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Db 1 MREENKMGPSGGSGDEGLASAAAGLVKVRQLLEAGADPNVNRFGRRRAIQVMMGSGAR 60
QY 1 MREENKMGPSGGSGDEGLATPA-RGLVEKVRHSEWAGADPNVNRFGRRRAIQVMMGSGAR 59
Db 61 VAEILLHGAEPNCADPATLTFRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLA 120
QY 60 VAEILLHGAEPNCADPATLTFRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLA 119
Db 121 EERGHDRVAGYLRTATGD 138
QY 120 EERGHDRVAGYLRTATGD 137

WPELEH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:38:35 2000; MapPar time 10.90 Seconds
592.803 Million cell updates/sec
Tabular output not generated.

Title: >US-09-016-869A-4
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Perfect Score: 977
Sequence: 1 MREENKMGPMGGSGDEGLAT.....LAERGRHVDVAGYLRTATGD 137

Scoring table: PAM 150
Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir63
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 42.515; Variance 86.121; scale 0.494

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
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2	749	76.7	130	2	p15INK4b - mouse	3.56e-123
3	692	70.8	156	2	J20141 cyclin dependent kina	1.22e-111
4	581	59.5	167	2	I58352 p16INK4a - mouse	2.36e-89
5	329	33.7	164	2	A57378 cyclin-dependent kina	3.08e-40
6	315	32.2	166	2	A57379 CDK4/CDK6 inhibitor p	1.30e-37
7	312	31.9	166	2	B57378 cyclin-dependent kina	4.74e-37
8	284	29.1	41	2	I52720 gene p15INK4B protein	7.40e-32
9	249	25.5	168	2	A55479 CDK6 inhibitor p18 -	1.74e-25
10	247	25.3	168	2	B57379 CDK4/CDK6 inhibitor p	3.99e-25
11	140	14.3	1423	1	I37275 death-associated prot	4.79e-07
12	140	14.3	1856	2	B35049 ankryrin 1, erythrocyt	4.79e-07
13	140	14.3	1880	2	A35049 ankryrin 1, erythrocyt	4.79e-07
14	140	14.3	1881	1	S3HUK ankryrin 1, erythrocyt	4.79e-07
15	137	14.0	1848	2	I37771 ankryrin, erythrocyte	1.38e-06
16	137	14.0	1862	2	I49502 ankryrin - mouse	1.38e-06
17	133	13.6	2524	2	A35844 xotch protein - Afric	5.56e-06
18	132	13.5	4377	2	A35575 ankryrin 3, long splic	7.86e-06
19	131	13.4	3924	2	S37431 ankryrin 2, neuronal	1.11e-05
20	130	13.3	2531	2	S18188 notch protein homolog	1.56e-05
21	129	13.2	1411	2	S30355 alpha-latroinsectotox	2.20e-05
22	129	13.2	2318	2	S45306 notch 3 protein - mou	2.20e-05
23	129	13.2	2555	2	A40043 notch protein homolog	2.20e-05

24	128	13.1	2437	2	S42612 transmembrane protein	3.10e-05
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26	125	12.8	2531	2	A46019 Notch-1 protein - mou	8.58e-05
27	123	12.6	638	2	A56695 notch2 protein homolo	1.68e-04
28	123	12.6	249128	2	A49128 cell-fate determining	1.68e-04
29	122	12.5	677	2	I49045 SKD3 - mouse	2.35e-04
30	121	12.4	209	2	T15888 hypothetical protein	3.27e-04
31	118	12.1	323	2	B47159 ankryrin-like repeat p	8.82e-04
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33	115	11.8	414	2	A53950 transcription factor	2.35e-03
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43	108	11.1	446	2	A34794 B-cell CLL/lymphoma 3	2.19e-02
44	106	10.8	1549	2	T13940 ankryrin - fruit fly	4.09e-02
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DATE		23-Mar-1995	#sequence_revision 23-Mar-1995
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#authors		Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Xiong, Y.	
#journal		Genes Dev. (1994) 8:2939-2952	
#title		Growth suppression by p18, a p16(INK4/MTS1)- and p14 (INK4B/MTS2)-related CDK6 inhibitor, correlates with wild-type pRB function.	
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#authors		Hannon, G.J.; Beach, D.	
#journal		Nature (1994) 371:257-261	
#title		p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.	
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#authors		Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.; Johnson, B.E.; Skolnick, M.H.	
#journal		Science (1994) 264:436-440	
#title		A cell cycle regulator potentially involved in genesis of many tumor types.	
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Papadopoulos, N.; Markowitz, S.; Willson, J.K.; Kinzler,
K.W.; Vogelstein, B.
#journal      Cancer Res. (1994) 54:6353-6358
#title        Deletion of p16 and p15 genes in brain tumors.
#cross-references MUID:95079408
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#map_position 9p21-9p21
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SUMMARY       #length 138 #molecular-weight 14722 #checksum 1236
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Best Local Similarity 95.7%; Pred. No. 7.51e-158;
Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
Db 1 MREENKMGSGSDGLAARGVLEKVRQLLEAGDPNGVNRFGRRRAIQVMMGSGAR 60
QY 1 MREENKMGSGSDGLATPA-RGLVKRVSWEGADPNVNRFGRRRAIQVMMGSGAR 59
Db 61 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVHLHAGARLDVDRAGRLPVDLA 120
QY 60 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVHLHAGARLDVDRAGRLPVDLA 119
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28-Feb-1997
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REFERENCE   178845 #status preliminary
#authors    Queller, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.;
Trono, D.; Richter, K.H.; Walker, C.; Beach, D.; Sherr,
C.J.; Serrano, M.
#journal    Oncogene (1995) 11:635-645
#title      Cloning and characterization of murine p16INK4a and p15INK4b
genes.
#cross-references MUID:95380169
#accession  178845
#molecule_type mRNA
#residues   1-130 ##label RES
#cross-references GB:S79252; NID:gl087092; PID:gl087093
GENETICS
#gene       p15INK4b
SUMMARY     #length 130 #molecular-weight 13788 #checksum 7879
Query Match   76.7%; Score 749; DB 2; Length 130;
Best Local Similarity 85.2%; Pred. No. 3.56e-123;
Matches 109; Conservative 11; Mismatches 7; Indels 1; Gaps 1;
Db 3 GGSDDAGLATAARGQVETVROLLEAGDPNALNFRGRRPIQVMMGSAQVAELLLHGA 62
QY 11 GGSDEGLATPA-RGLVKRVSWEGADPNVNRFGRRRAIQVMMGSAQVAELLLHGA 69
Db 63 EPNCADPATLTPRVHDAAREGFLDTLVHLHAGARLDVCDWAGRLPVDLAEEQGHDR 122
QY 70 EPNCADPATLTPRVHDAAREGFLDTLVHLHAGARLDVCDWAGRLPVDLAEEQGHDR 129
Db 123 YLHAATGD 130
```

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QY 130 YLRTATGD 137
|||||
RESULT 3
ENTRY   JE0141 #type complete
TITLE   cyclin dependent kinase - human
ALTERNATE_NAMES CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase
inhibitor 2A; multiple tumor suppressor 1 (MTS1)
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change
26-Aug-1999
ACCESSIONS JE0141; I59268; S39359; I59585; JC5679
REFERENCE   JE0141
#authors    Huang, C.G.; Deng, W.; Fu, J.L.
#journal    Chinese J. Biotechnol. (1997) 13:105-107
#title      Molecular cloning and sequencing of p16ink4 cDNA from hela
cell.
#accession  JE0141
#molecule_type mRNA
#residues   1-156 ##label HUA
#experimental_source Hella cell
REFERENCE   I59268
#authors    Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.;
Serrano, M.; Bennett, W.P.; Forrester, K.; Gerwin, B.;
Hussain, S.P.; Beach, D.H.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:11045-11049
#title      Mutations and altered expression of p16INK4 in human cancer.
#cross-references MUID:95062202
#accession  I59268
#status     translation not shown; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues   1-152 ##label RES
#cross-references GB:S74232; NID:g710467
#note       this report is a correction
REFERENCE   S39359
#authors    Serrano, M.; Hannon, G.J.; Beach, D.
#journal    Nature (1993) 366:704-707
#title      A new regulatory motif in cell-cycle control causing specific
inhibition of cyclin D/CDK4.
#cross-references MUID:94081956
#accession  S39359
#status     preliminary
#molecule_type mRNA
#residues   9-34, 'V' 36-156 ##label SER
#note       this sequence has been corrected in reference I59268
REFERENCE   I59585
#authors    Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.;
Harshman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.;
Johnson, B.E.; Skolnick, M.H.
#journal    Science (1994) 264:436-440
#title      A cell cycle regulator potentially involved in genesis of
many tumor types.
#cross-references MUID:94204645
#accession  I59585
#status     translation not shown; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues   51-152 ##label RE2
#cross-references GB:S69804; NID:g546272
REFERENCE   JC5679
#authors    Huang, C.; Deng, W.; Fu, J.
#journal    Chinese J. Biotechnol. (1997) 13:105-107
#title      Molecular cloning and sequencing of p16 ink4 cDNA from hela
cell.
#accession  JC5679
#molecule_type mRNA
#residues   1-156 ##label HU2
#note       This protein suppresses the function of cyclin D1/CDK4 and cyclin
D1/CDK6.
GENETICS
#gene       p16ink4; MLM; CDKN2; MTS1
#cross-references GDB:335362; GDB:CDKN2A; OMIM:600160
#map_position 9p21-9p21
```

```
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins
KEYWORDS cell cycle control; protein kinase inhibitor; tumor
suppressor
SUMMARY #length 156 #molecular-weight 16532 #checksum 6490

Query Match 70.8%; Score 692; DB 2; Length 156;
Best Local Similarity 85.8%; Pred. No. 1.22e-111;
Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Db 16 LATAAARGVEVTRALLEAGALPNASVGRRIQVMMGSAARVAELLHGAEPNCADP 75
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18 LATPA-RGLVEKVRHSWEAGADPNVGRRAIQVMMGSAARVAELLHGAEPNCADP 76
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 ATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAERGHDRVAYLRAAG 135
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 ATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAERGHDRVAGYLRTATG 136
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
ENTRY I58352 #type complete
TITLE p16INK4a - mouse
ORGANISM #formal_name Mus sp. #common_name mouse
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
ACCESSIONS I58352
REFERENCE I58352
#authors Quella, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.;
Trono, D.; Richter, K.H.; Walker, C.; Beach, D.; Sherr,
C.J.; Serrano, M.
#journal Oncogene (1995) 11:635-645
#title Cloning and characterization of murine p16INK4a and p15INK4b
#cross-references MUID:95380169
#accession I58352
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-167 #label RES
#cross-references GB:S79251; NID:g1087090; PID:g1087091
GENETICS
#gene p16INK4a
SUMMARY #length 167 #molecular-weight 17870 #checksum 1257

Query Match 59.5%; Score 581; DB 2; Length 167;
Best Local Similarity 65.6%; Pred. No. 2.36e-89;
Matches 80; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

Db 3 SAADRLAAQGRVHDVRLLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLINYGADSN 62
::: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 13 GSDEGLATPARGLVKVRHSWEAGADPNVGRRAIQVMMGSAARVAELLHGAEPN 72
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 CEDPTTFSRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPDLAERGHODIVRYLR 122
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 73 CADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPDLAERGHDRVAGYL 132
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123 SA 124
QY 133 TA 134

RESULT 5
ENTRY A57378 #type complete
TITLE cyclin-dependent kinase inhibitor p19 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
22-Jun-1999
ACCESSIONS A57378
REFERENCE A57378
#authors Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
#journal Mol. Cell. Biol. (1995) 15:2682-2688
#title Identification of human and mouse p19, a novel CDK4 and CDK6
inhibitor with homology to p16(ink4).
#cross-references MUID:95257949
#accession A57378
```

```
#status preliminary
#molecule_type mRNA
#residues 1-164 #label CHA
#cross-references GB:U20498
GENETICS
#map_position 19p13
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
SUMMARY #length 164 #molecular-weight 17362 #checksum 5271

Query Match 33.7%; Score 329; DB 2; Length 164;
Best Local Similarity 46.6%; Pred. No. 3.08e-40;
Matches 55; Conservative 23; Mismatches 38; Indels 2; Gaps 2;

Db 13 GAAARGDQVEVRLLHRELHPDANRFKTAIQVMFGSTALQLKQASPNVQDAS 72
::: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 19 ATPARGLVKVRHSWEAG-ADPNVGRRAIQVMMGSAARVAELLHGAEPNCADPA 77
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 73 G-TSPVHDAARTGFLDTLVVLRHAGARLDVDAWGRLPVDLAERGHDRVAGYLRAES 129
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 78 TLTRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAERGHDRVAGYLRTAT 135
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
ENTRY A57379 #type complete
TITLE CDK4/CDK6 inhibitor p19 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
20-Sep-1999
ACCESSIONS A57379
REFERENCE A57379
#authors Hirai, H.; Rousset, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr,
C.J.
#journal Mol. Cell. Biol. (1995) 15:2672-2681
#title Novel INK4 proteins, p19 and p18, are specific inhibitors of
the cyclin D-dependent kinases CDK4 and CDK6.
#cross-references MUID:95257948
#accession A57379
#status preliminary
#molecule_type mRNA
#residues 1-166 #label HIR
#cross-references GB:U19597; NID:g790568; PID:AC52194.1; PID:g790569
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
KEYWORDS cell cycle control
SUMMARY #length 166 #molecular-weight 17894 #checksum 3512

Query Match 32.2%; Score 315; DB 2; Length 166;
Best Local Similarity 48.2%; Pred. No. 1.30e-37;
Matches 55; Conservative 19; Mismatches 38; Indels 2; Gaps 2;

Db 14 GARARGDQVEVRLLHRELHPDANRFKTAIQVMFGSPAVALLELLKQASPNVQDAS 73
::: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY 19 ATPARGLVKVRHSWEAG-ADPNVGRRAIQVMMGSAARVAELLHGAEPNCADPA 77
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 74 G-TSPVHDAARTGFLDTLVVLRHAGARLDVDAWGRLPVDLAERGHDSVSWFL 126
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 78 TLTRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAERGHDRVAGYL 131
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
ENTRY B57378 #type complete
TITLE cyclin-dependent kinase inhibitor p19 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
20-Sep-1999
ACCESSIONS B57378
REFERENCE B57378
#authors Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
#journal Mol. Cell. Biol. (1995) 15:2682-2688
#title Identification of human and mouse p19, a novel CDK4 and CDK6
inhibitor with homology to p16(ink4).
#cross-references MUID:95257949
```

```

#accession B57378 #molecule_type preliminary
#status 1-166 #label CHA
#residues 1-166 #label CHA
#cross-references GB:U20497; NID:G791204; PIDN:AA085437.1; PID:G791205
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
SUMMARY #length 166 #molecular-weight 17920 #checksum 3767

Query Match 31.9%; Score 312; DB 2; Length 166;
Best Local Similarity 47.4%; Pred. No. 4.74e-37;
Matches 54; Conservative 20; Mismatches 38; Indels 2; Gaps 2;

Db 14 GARGDQVQVRLRLHRLVHPDNLNRGKALQVMMFGSPAVALELLKQASPNVQDAS 73
QY 19 ATPARGLVKVRHWEAG-ADPNQVNRGRRRAIQVMMGSRVAEALLLHGAEPNCADPA 77
Db 74 G-TSPVHDAARTGTDTLTKLVHAGADYNALDSTGSLPIHLAIREGHSSVVSFL 126
QY 78 TLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAERGHDRVAGYL 131

RESULT 8
ENTRY #type fragment
TITLE gene p15INK4B protein - rat (fragment)
ORGANISM #formal_name Rattus sp. #common_name rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS I52720
REFERENCE #molecule_type DNA
#authors Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.
#journal Cancer Res. (1995) 55:1607-1612
#title Association of rat p15INK4B/p16INK4 deletions with monosomy 5
in kidney epithelial cell lines but not primary renal
tumors.
#cross-references MUID:95228036
#accession I52720
#status preliminary; translated from GB/EMBL/DBJ
#residues 1-41 #label RES
#cross-references GB:S77734; NID:G998711
GENETICS
#gene p15INK4B
#length 41 #checksum 3296
SUMMARY
Query Match 29.1%; Score 284; DB 2; Length 41;
Best Local Similarity 97.6%; Pred. No. 7.40e-32;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGSAQVAELLLHGAEPNCADPATLTPVHDAAREGFLD 41
QY 53 MMGSAQVAELLLHGAEPNCADPATLTPVHDAAREGFLD 93

RESULT 9
ENTRY #type complete
TITLE CDK6 inhibitor p18 - human
ALTERNATE_NAMES cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent
kinase CDK6 inhibitor p18
ORGANISM #formal_name Homo sapiens #common_name man
DATE 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
ACCESSIONS A55479
REFERENCE #molecule_type mRNA
#authors Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.;
O'Keefe, C.L.; Matera, A.G.; Xiong, Y.
#journal Genes Dev. (1994) 8:2939-2952
#title Growth suppression by p18, a p16(INK4A/MTS1)- and p14
(INK4B/MTS2)-related CDK6 inhibitor, correlates with
wild-type pRB function.
#cross-references MUID:95095079
#accession A55479
#molecule_type mRNA

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#residues 1-168 #label GUA
#cross-references GB:U17074; NID:G639713; PIDN:AA050074.1; PID:G639714
GENETICS
#gene GDB:CDKN2C
#cross-references GDB:594931
#map_position lp32-lp32
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
cell cycle control; protein kinase inhibitor; tumor
suppressor
SUMMARY #length 168 #molecular-weight 18127 #checksum 9379

Query Match 25.5%; Score 249; DB 2; Length 168;
Best Local Similarity 39.0%; Pred. No. 1.74e-25;
Matches 46; Conservative 28; Mismatches 43; Indels 1; Gaps 1;

Db 6 GNELASAAAGDLEOLTSLQNNVNAONGFGRALQVMMKLGNPETARLLLRGANPDL 65
QY 14 SDEGLATPARGLVKVRHWEAGADPNQVNRGRRRAIQVMMGSRVAEALLLHGAEPNC 73
Db 66 KDTGTGA-VIHDAAAGFLDTLQTLLEFQADVNIENEGNPLHLAAKEGHLRVVEFL 122
QY 74 ADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAERGHDRVAGYL 131

RESULT 10
ENTRY #type complete
TITLE CDK4/CDK6 inhibitor p18 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
ACCESSIONS B57379
REFERENCE #molecule_type mRNA
#authors Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr,
C.J.
#journal Mol. Cell. Biol. (1995) 15:2672-2681
#title Novel INK4 proteins, p19 and p18, are specific inhibitors of
the cyclin D-dependent kinases CDK4 and CDK6.
#cross-references MUID:95257948
#accession B57379
#status preliminary
#molecule_type mRNA
#residues 1-168 #label HIR
#cross-references GB:U19396; PIDN:G790566; PIDN:AA052193.1; PID:G790567
CLASSIFICATION #superfamily unassigned ankryrin repeat proteins; ankryrin
repeat homology; EGF homology
cell cycle control
SUMMARY #length 168 #molecular-weight 18066 #checksum 8831

Query Match 25.3%; Score 247; DB 2; Length 168;
Best Local Similarity 38.2%; Pred. No. 3.99e-25;
Matches 47; Conservative 29; Mismatches 46; Indels 1; Gaps 1;

Db 6 GNELASAAAGDLEOLTSLQNNVNAONGFGRALQVMMKLGNPETARLLLRGANPDL 65
QY 14 SDEGLATPARGLVKVRHWEAGADPNQVNRGRRRAIQVMMGSRVAEALLLHGAEPNC 73
Db 66 KDTGTGA-VIHDAAAGFLDTLQTLLEFQADVNIENEGNPLHLAAKEGHLRVVEFLM 124
QY 74 ADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAERGHDRVAGYLRT 133
Db 125 HTA 127
QY 134 ATG 136

RESULT 11
ENTRY #type complete
TITLE death-associated protein kinase (EC 2.7.1.-) - human
ALTERNATE_NAMES calmodulin-dependent protein kinase homolog; DAP kinase
ORGANISM #formal_name Homo sapiens #common_name man
DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
10-Jul-1998

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ACCESSIONS      I37275; S39269
REFERENCE        A55614
#authors        Deliss, L.P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi, A.
#journal         Genes Dev. (1995) 9:15-30
#title          Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell death.
#cross-references MUID:95129831
#accession      I37275
#molecule_type mRNA
#residues       1-1423 #label RES
#cross-references EMBL:X76104; NID:g434846; PID:g434847
GENETICS
#gene           GDB:DAPK1; DAPK
#cross-references GDB:555932; OMIM:600831
#map_position   9q34.1-9q34.1
#description    catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate using ATP
#pathway        apoptosis
#note           activity is calmodulin dependent
#superfamily    death-associated protein kinase; ankyrin repeat
#CLASSIFICATION
#keywords       apoptosis; ATP; calmodulin binding; phosphotransferase; serine/threonine-specific protein kinase; tandem repeat
FEATURE
11-267          #domain protein kinase homology #label KIN
19-27           #region protein kinase ATP-binding motif
285-308         #region calmodulin binding status predicted
370-402         #domain ankyrin repeat homology #label AN1
403-435         #domain ankyrin repeat homology #label AN2
436-468         #domain ankyrin repeat homology #label AN3
470-502         #domain ankyrin repeat homology #label AN4
503-535         #domain ankyrin repeat homology #label AN5
536-568         #domain ankyrin repeat homology #label AN6
569-601         #domain ankyrin repeat homology #label AN7
602-634         #domain ankyrin repeat homology #label AN8
42,64,139,141  #active_site Lys, Glu, Asp, Lys #status predicted
SUMMARY        #length 1423 #molecular-weight 159161 #checksum 6280
Query Match    14.38; Score 140; DB 1; Length 1423;
Best Local Similarity 32.28; Pred. No. 4.79e-07;
Matches 37; Conservative 23; Mismatches 53; Indels 2; Gaps 2;
Db 509 LTASRGYHDIVCLAEHGDADLNACDKDGHIALHLAYRCOMEYIKTLSSQGCFFDYQDR 568
QY 18 LATPARGLVKVRHSWEAGADPNGVNRFRRAIQVMMGNSAR-VAELLHLLHGAEPNCADP 76
Db 569 HGNT-PLHVACKDGNMIPVALCEANCNLDISNKYGRTPPLHLAANGILDVRYL 622
QY 77 ATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAERGHDRDVAGYL 131
RESULT 12
ENTRY          B35049 #type complete
TITLE          ankyrin 1, erythrocyte splice form 3 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS       ankyrin 2.2, erythrocyte
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
ACCESSIONS     B35049
REFERENCE       Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
#journal        Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
#title          CDNA sequence for human erythrocyte ankyrin.
#cross-references MUID:90175370
#accession      B35049
#status         preliminary
#molecule_type mRNA
#residues       1-1856 #label LAM

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GENETICS
#gene           GDB:ANK1; ANK
#cross-references GDB:118737; OMIM:182900
#map_position    8p11.2-8p11.2
#CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
#KEYWORDS        alternative splicing
FEATURE
2-1856          #product ankyrin 1, erythrocyte form 3 #status predicted
                #label MAR
                #product ankyrin 2.2, erythrocyte #status predicted
                #label MA2
44-76           #domain ankyrin repeat homology #label ANO1
77-109          #domain ankyrin repeat homology #label ANO2
110-142         #domain ankyrin repeat homology #label ANO3
143-171         #domain ankyrin repeat homology #label ANO4
172-204         #domain ankyrin repeat homology #label ANO5
205-237         #domain ankyrin repeat homology #label ANO6
238-270         #domain ankyrin repeat homology #label ANO7
271-303         #domain ankyrin repeat homology #label ANO8
304-336         #domain ankyrin repeat homology #label ANO9
337-369         #domain ankyrin repeat homology #label ANO10
370-402         #domain ankyrin repeat homology #label ANO11
403-435         #domain ankyrin repeat homology #label ANO12
436-468         #domain ankyrin repeat homology #label ANO13
469-501         #domain ankyrin repeat homology #label ANO14
502-534         #domain ankyrin repeat homology #label ANO15
535-567         #domain ankyrin repeat homology #label ANO16
568-600         #domain ankyrin repeat homology #label ANO17
601-633         #domain ankyrin repeat homology #label ANO18
634-666         #domain ankyrin repeat homology #label ANO19
667-699         #domain ankyrin repeat homology #label ANO20
700-732         #domain ankyrin repeat homology #label ANO21
733-765         #domain ankyrin repeat homology #label ANO22
766-798         #domain ankyrin repeat homology #label ANO23
SUMMARY        #length 1856 #molecular-weight 203445 #checksum 6521
Query Match    14.38; Score 140; DB 2; Length 1856;
Best Local Similarity 32.38; Pred. No. 4.79e-07;
Matches 42; Conservative 25; Mismatches 55; Indels 8; Gaps 8;
Db 493 NAMPNLATTAG-HTPLHIAAREGHVETVLALLEKEASQACMTKGTPLHVAARYKVRV 551
QY 3 EENKMPGSGGSDEGLATPAR-GLVEKVRHSWEAGADPNGVNRFRRAIQVMM-GSARV 60
Db 552 AELLERDAHPNAGKNLT-PLHVAHVHNNLDIVKLLPRGGSP-HSP-AWNGYTPLHI 608
QY 61 AEILLHGAEPNCADPATLRPVHDAAREGFLDTL-VVLRHAGARLDVRDAG-GRLPVDL 118
Db 609 AAKQNOVEVA 618
QY 119 AEERGHDRVA 128
RESULT 13
ENTRY          A35049 #type complete
TITLE          ankyrin 1, erythrocyte splice form 2 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS       ankyrin 2.2, erythrocyte
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
ACCESSIONS     A35049
REFERENCE       Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
#journal        Proc. Natl. Acad. Sci. U.S.A. (1990) 87:1730-1734
#title          CDNA sequence for human erythrocyte ankyrin.
#cross-references MUID:90175370
#accession      A35049
#status         preliminary
#molecule_type mRNA
#residues       1-1880 #label LAM
#cross-references GB:M28880

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GENETICS
#gene GDB:ANK1; ANK
#cross-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS #alternative splicing; cytoskeleton
FEATURE
2-1880
#product ankyrin 1, erythrocyte form 2 #status predicted
#label MAT1
#product ankyrin 2.2, erythrocyte #status predicted
#label MA2
#domain ankyrin repeat homology #label AN01
#domain ankyrin repeat homology #label AN02
#domain ankyrin repeat homology #label AN03
#domain ankyrin repeat homology #label AN04
#domain ankyrin repeat homology #label AN05
#domain ankyrin repeat homology #label AN06
#domain ankyrin repeat homology #label AN07
#domain ankyrin repeat homology #label AN08
#domain ankyrin repeat homology #label AN09
#domain ankyrin repeat homology #label AN10
#domain ankyrin repeat homology #label AN11
#domain ankyrin repeat homology #label AN12
#domain ankyrin repeat homology #label AN13
#domain ankyrin repeat homology #label AN14
#domain ankyrin repeat homology #label AN15
#domain ankyrin repeat homology #label AN16
#domain ankyrin repeat homology #label AN17
#domain ankyrin repeat homology #label AN18
#domain ankyrin repeat homology #label AN19
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#length 1880 #molecular-weight 206066 #checksum 6968

SUMMARY
Query Match 14.3%; Score 140; DB 2; Length 1880;
Best Local Similarity 32.3%; Pred. No. 4.79e-07;
Matches 42; Conservative 25; Mismatches 55; Indels 8; Gaps 8;

Db 493 NANPNLATAG-HTPLHIAAREGHVETVLLLEKASQACMTKKGFTPLHVAAKYGVKV 551
QY 3 ENKGMPSGGSGDEGLATPAR-GLVEKVRHSWEAGDPNGVNFERRAIQVMM-GSARV 60

Db 552 AELLERDAPNAKNGKIT-PLHVAVHNNLDIVKLLPRGGSP-HSP-AWNGYTPLHI 608
QY 61 AELLHGAEPNCADPATLTPVDAARSGFDTL-VLHRAGAKLDVRDAW-GRLPVDL 118

Db 609 AAKQNOVEVA 618
QY 119 AEERGHDRVA 128

RESULT 14
ENTRY SUHUK #type complete
TITLE ankyrin 1, erythrocyte splice form 1 - human
ALTERNATE_NAMES ankyrin 2.1, erythrocyte; ankyrin-R
CONTAINS ankyrin 2
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
22-Jun-1999

ACCESSIONS S08275; A33219; PC2220; A35443
REFERENCE S08275
#authors Lux, S.E.; John, K.M.; Bennett, V.
#journal Nature (1990) 344:36-42
#title Analysis of cDNA for human erythrocyte ankyrin indicates a
repeated structure with homology to tissue-differentiation
and cell-cycle control proteins.
#cross-references MUID:90158830
#accession S08275
#molecule_type mRNA
#residues 1-1881 #label LU1
#cross-references EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702

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#accession A33219
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#residues 2-7,'X',9-17,'X',19-20,'T',22-30:733-749,'A',751-753;
828-833,'X',835-855,'X',857-859,'XX',862-871;959-1003;
1106-1120,'XX',1123-1128;1149-1172:1282-1285,'R',
1287-1288;1307-1332:1345-1365,'X',1367:1383-1427;
1601-1630:1686-1698,'D',1700;1763-1772 #label L0X
845-Arg and 1392-Thr were also found

#note PC2220
REFERENCE
#authors Hermann, J.; Barel, M.; Frade, R.
#journal Biochem. Biophys. Res. Commun. (1994) 204:453-460
#title Human erythrocyte ankyrin, a cytoskeleton component,
generates the p57 membrane proteinase which cleaves C3, the
third component of complement.
#cross-references MUID:95071348
#accession PC2220
#molecule_type protein
#residues 910-929 #label HER
REFERENCE
#authors Davis, L.H.; Bennett, V.
#journal J. Biol. Chem. (1990) 265:10589-10596
#title Mapping the binding sites of human erythrocyte ankyrin for
the anion exchanger and spectrin.
#cross-references MUID:90285190
#accession A35443
#molecule_type protein
#residues 'X',5,'X',7-12:403-417,'X',419-422,'H',424,'LQ',797-800,
'L',802-814;862-863,'X',865-877,'X',899-901,'T',
903-909,'X',911-912 #label DAV

GENETICS
#gene GDB:ANK1; ANK
#cross-references GDB:118737; OMIM:182900
#map_position 8p11.2-8p11.2
CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS #alternative splicing; phosphoprotein
FEATURE
2-1881
#product ankyrin 1, erythrocyte form 1 #status predicted
#label MAT1
#product ankyrin 2.2, erythrocyte #status predicted
#label MA2
#domain 89K #status predicted #label DOM1
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#domain ankyrin repeat homology #label AN01
#domain ankyrin repeat homology #label AN02
#domain ankyrin repeat homology #label AN03
#domain ankyrin repeat homology #label AN04
#domain ankyrin repeat homology #label AN05
#domain ankyrin repeat homology #label AN06
#domain ankyrin repeat homology #label AN07
#domain ankyrin repeat homology #label AN08
#domain ankyrin repeat homology #label AN09
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#domain ankyrin repeat homology #label AN11
#domain ankyrin repeat homology #label AN12
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#domain ankyrin repeat homology #label AN18
#domain ankyrin repeat homology #label AN19
#domain ankyrin repeat homology #label AN20
#domain ankyrin repeat homology #label AN21
#domain ankyrin repeat homology #label AN22
#domain 62K #status predicted #label DOM2
#region spectrin binding
#domain 55K #status predicted 206275 #checksum 2619
SUMMARY
Query Match 14.3%; Score 140; DB 1; Length 1881;
Best Local Similarity 32.3%; Pred. No. 4.79e-07;
Matches 42; Conservative 25; Mismatches 55; Indels 8; Gaps 8;

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Db 493 NANPLATTAG-HTPLHTAAREGHVETVLALLEKEASQACMTKGFTHLHVAKYKVRV 551
Qy 3 EENKMPGGSGDEGLATPAR-GLYKVRHSWEAGDPNGVNRFRRAIQVMM-GSARV 60
Db 552 AELLERDAHPNAGKNGLT-PLHVAVHNNDIVKLLPRGGSP-HSP-AWNGYTPLHI 608
Qy 61 AELLHGAEPNCADPATLTPRVHDAAREGFDTL-VVLRAGARLDVRDAW-GRLPVDL 118
Db 609 AAKQNQVEVA 618
Qy 119 AEERGHDRVA 128

RESULT 15
ENTRY S37771 #type complete
TITLE ankyrin, erythrocyte - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999

ACCESSIONS S37771
REFERENCE S37771
#authors Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
#journal J. Biol. Chem. (1993) 268:9533-9540
#title Complex patterns of sequence variation and multiple 5' and 3' ends are found among transcripts of the erythroid ankyrin gene.

#cross-references MUID:93252825
#accession S37771
#status preliminary
#molecule_type mRNA
#residues 1-1848 #label BIR
#cross-references EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817

CLASSIFICATION #superfamily ankyrin; ankyrin repeat homology
KEYWORDS alternative splicing
FEATURE
48-80 #domain ankyrin repeat homology #label AN01\
81-113 #domain ankyrin repeat homology #label AN02\
114-146 #domain ankyrin repeat homology #label AN03\
147-175 #domain ankyrin repeat homology #label AN04\
176-208 #domain ankyrin repeat homology #label AN05\
209-241 #domain ankyrin repeat homology #label AN06\
242-274 #domain ankyrin repeat homology #label AN07\
275-307 #domain ankyrin repeat homology #label AN08\
308-340 #domain ankyrin repeat homology #label AN09\
341-373 #domain ankyrin repeat homology #label AN10\
374-406 #domain ankyrin repeat homology #label AN11\
407-439 #domain ankyrin repeat homology #label AN12\
440-472 #domain ankyrin repeat homology #label AN13\
473-505 #domain ankyrin repeat homology #label AN14\
506-538 #domain ankyrin repeat homology #label AN15\
539-571 #domain ankyrin repeat homology #label AN16\
572-604 #domain ankyrin repeat homology #label AN17\
605-637 #domain ankyrin repeat homology #label AN18\
638-670 #domain ankyrin repeat homology #label AN19\
671-703 #domain ankyrin repeat homology #label AN20\
704-736 #domain ankyrin repeat homology #label AN21\
737-769 #domain ankyrin repeat homology #label AN22\
770-802 #domain ankyrin repeat homology #label AN23
SUMMARY #length 1848 #molecular_weight 202576 #checksum 2542

Query Match 14.0%; Score 137; DB 2; Length 1848;
Best Local Similarity 33.9%; Pred. No. 1.38e-06;
Matches 39; Conservative 21; Mismatches 48; Indels 7; Gaps 7;

Db 511 LHTAREGHVDTALLLEKEASQACMTKGFTHLHVAKYKVRVLAELLLEHDAHPNAG 570
Qy 18 LATPAR-GLYKVRHSWEAGDPNGVNRFRRAIQVMM-GSARVLAELLHGAEPNCAD 75
Db 571 KNGLT-PLHVAVHNNDIVKLLPRGGSP-HSP-AWNGYTPLHTAAKQNQVEVA 622

Qy 76 PATLTPRVHDAAREGFDTL-VVLRAGARLDVRDAW-GRLPVDLAEERGHDRVA 128
Search completed: Thu Jul 20 08:38:48 2000
Job time : 13 secs.

MPSRELH
(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Jul 20 08:39:06 2000; MasPar time 6.93 Seconds
Tabular output not generated. 602.124 Million cell updates/sec

Title: >US-09-016-869A-4
Description: (1-137) from US09016869A.pep
Perfect Score: 977
Sequence: 1 MREENKMGPGSGSDEGLAT.....LAERGHDRVAGYLRTATGD 137

Scoring table: PAM 150
Gap 11

Searched: 83857 segs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 43.541; Variance 77.735; scale 0.560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description	Pred. No.
1	919	94.1	138	1	CDN5_HUMAN	CYCLIN-DEPENDENT KINAS 7.32e-179
2	751	76.9	130	1	CDN5_RAT	CYCLIN-DEPENDENT KINAS 4.85e-140
3	749	76.7	130	1	CDN5_MOUSE	CYCLIN-DEPENDENT KINAS 1.40e-139
4	692	70.8	156	1	CDN2_HUMAN	CYCLIN-DEPENDENT KINAS 1.62e-126
5	581	59.5	167	1	CDN2_MOUSE	CYCLIN-DEPENDENT KINAS 2.75e-101
6	572	58.5	171	1	CDN2_MONDO	CYCLIN-DEPENDENT KINAS 2.96e-99
7	329	33.7	166	1	CDN7_HUMAN	CYCLIN-DEPENDENT KINAS 9.77e-46
8	315	32.2	166	1	CDN7_MOUSE	CYCLIN-DEPENDENT KINAS 9.05e-43
9	249	25.5	168	1	CDN6_HUMAN	CYCLIN-DEPENDENT KINAS 4.38e-29
10	247	25.3	168	1	CDN6_MOUSE	CYCLIN-DEPENDENT KINAS 1.11e-28
11	140	14.3	1431	1	DAPK_HUMAN	DEATH-ASSOCIATED PROTE 2.39e-08
12	140	14.3	1880	1	ANKK_HUMAN	ANKYRIN R (ANKYRINS 2. 2.39e-08
13	137	14.0	1862	1	ANKL_MOUSE	ANKYRIN. 7.81e-08
14	133	13.6	2524	1	NOTC_XENLA	NEUROGENIC LOCUS NOTCH 3.72e-07
15	131	13.4	1839	1	ANKB_HUMAN	ANKYRIN, BRAIN VARIANT 8.05e-07
16	131	13.4	3924	1	ANKC_HUMAN	ANKYRIN, BRAIN VARIANT 8.05e-07
17	130	13.3	2531	1	NTCL_RAT	NEUROGENIC LOCUS NOTCH 1.18e-06
18	129	13.2	2318	1	NTC3_MOUSE	NEUROGENIC LOCUS NOTCH 1.73e-06
19	129	13.2	2444	1	NTCL_HUMAN	NEUROGENIC LOCUS NOTCH 1.73e-06
20	128	13.1	2437	1	NOTC_BRARE	NEUROGENIC LOCUS NOTCH 2.54e-06
21	125	12.8	2531	1	NTCL_MOUSE	NEUROGENIC LOCUS NOTCH 7.91e-06
22	122	12.5	677	1	SKD3_MOUSE	SKD3 PROTEIN. 2.43e-05
23	121	12.4	2703	1	NOTC_DROME	NEUROGENIC LOCUS NOTCH 3.53e-05

CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC
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CC
CC ENBL; U17075; AAC50075.1; -;
CC ENBL; L36844; AAA50282.1; -;
CC ENBL; S69805; AAD14049.1; -;
CC MM; 600431; -;
CC Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation.
CC DOMAIN 13 103
CC REPEAT 13 39 2 X ANK MOTIF REPEATS.
CC REPEAT 73 103 ANK MOTIF 1 (INCOMPLETE).
CC VARIAT 47 47 ANK MOTIF 2.
CC G -> E (IN LUNG ADENOCARCINOMA).
CC /FTID-VAR_001488.
CC A -> V (IN LUNG ADENOCARCINOMA).
CC /FTID-VAR_001489.
CC SA -> TP (IN REF. 2).
CC MISSING (IN REF. 2).
CC OLL -> HSW (IN REF. 2).
CC SEQUENCE 138 AA; 14722 MW; 0D6FFBFA6FEAD21 CRC64;
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Matches 132; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
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Qy 1 MREKNGPSSGGSGDEGLATFA-RLGVEKVRHSWEAGADPNVGRFGRRAIQVMMGSGAR 59
Db 61 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLA 120
Qy 60 VAEILLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLA 119
Db 121 BERGRDVGILRTATGD 138
Qy 120 BERGRDVGILRTATGD 137
RESULT 2
ID CDN5_RAT STANDARD; PRT; 130 AA.
AC P55272;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
GN CDKN2B OR INK4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96001392.
RA Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
RA Tsuchiya H., Kikuchi Y., Mitani H.;
RT "Molecular genetic basis of renal carcinogenesis in the Eker rat
RT model of tuberous sclerosis (Tsc2).";
RL Mol. Carcinog. 14:23-27(1995).
RN [2]
RP SEQUENCE OF 46-86 FROM N.A.
RX MEDLINE; 95228036.
RA Knapik D.F., Serrano M., Beach D., Trono D., Walker C.L.;
RT "Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in
RT kidney epithelial cell lines but not primary renal tumors.";

RL Cancer Res. 55:1607-1612(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; S79760; AAB35360.1; -;
CC ENBL; S77734; CAB33639.1; -;
CC PFAM; PF00023; ank; 3.
CC Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CC CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT LONG FORM.
FT CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT SHORT FORM.
FT INIT_MET 46 46 FOR THE SHORT FORM.
FT DOMAIN 5 95 2 X ANK MOTIF REPEATS.
FT REPEAT 5 31 ANK MOTIF 1 (INCOMPLETE).
FT REPEAT 65 95 ANK MOTIF 2.
SQ SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;
Query Match 76.9%; Score 751; DB 1; Length 130;
Best Local Similarity 85.2%; Pred. No. 4.85e-140;
Matches 109; Conservative 11; Mismatches 7; Indels 1; Gaps 1;
Db 3 GGSDDAGLATAAARGQVETVRLLEAGADPNVGRFGRRAIQVMMGSAOVAELLHGA 62
Qy 11 GGSDEGLATPA-RLGVEKVRHSWEAGADPNVGRFGRRAIQVMMGSAOVAELLHGA 69
Db 63 EPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEEQGRDIAR 122
Qy 70 EPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAEEQGRDVAG 129
Db 123 YLHAATGD 130
Qy 130 YLRTATGD 137
RESULT 3
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AC P55271;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95380169.
RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RL Oncogene 11:635-645(1995).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J X DBA;
RX MEDLINE; 9732242.
RA Malumbres M., de Castro I., Santos J., Melendez B., Mangués R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RT "Inactivation of the cyclin-dependent kinase inhibitor p16INK4b by
RT deletion and de novo methylation with independence of p16INK4a
RT alterations in murine primary T-cell lymphomas.";
RL Oncogene 14:1361-1370(1997).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
CC -1- INDUCTION: BY TGF-BETA.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC -----
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CC -----
CC EMBL; U66085; AAB39833.1; -.
CC DR EMBL; U66084; AAB39833.1; JOINED.
CC DR MGD; MGI:104737; CDKN2B.
CC DR PFAM; PF00023; ank; 3.
CC KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.
CC FT DOMAIN 5 95 2 X ANK MOTIF REPEATS.
CC FT REPEAT 5 31 ANK MOTIF 1 (INCOMPLETE).
CC FT REPEAT 65 95 ANK MOTIF 2.
CC SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF52BCFF9 CRC64;
CC -----
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Best Local Similarity 85.2%; Pred. No. 1.40e-139;
Matches 109; Conservative 11; Mismatches 7; Indels 1; Gaps 1;
DB 3 GGSAGLATAAARGQVETVRLLEAGADPNALNRFRRTIQVNMGSAQVAELLHLGA 62
QY 11 GGSDEGLATPA-RGLVEKVRHSWEACADPNVNRFRGRRRAIQVNMGSAQVAELLHLGA 69
DB 63 EPCADPATITRPVHDAAEGFLDTLVLRHAGARLDVCDWGRLPVDLAEQGHRIAR 122
QY 70 EPCADPATITRPVHDAAEGFLDTLVLRHAGARLDVCDWGRLPVDLAEQGHRIAR 129
DB 123 YLHATGCD 130
QY 130 YLRTATGCD 137

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RP SEQUENCE OF 51-152 FROM N.A.
RX MEDLINE; 94204645.
RA Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
RA Skolnick M.H.;
RT "A cell cycle regulator potentially involved in genesis of many tumor
RT types.";
RL Science 264:436-440(1994).
RN [3]
RP SEQUENCE OF 1-20 FROM N.A.
RX MEDLINE; 96182088.
RA Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;
RT "Regulation of p16CDKN2 expression and its implications for cell
RT immortalization and senescence.";
RL Mol. Cell. Biol. 16:859-867(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
RX MEDLINE; 98421670.
RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;
RT "Structural basis for inhibition of the cyclin-dependent kinase Cdk6
RT by the tumour suppressor p16INK4a.";
RL Nature 395:237-243(1998).
RN [5]
RP REVIEW ON MELANOMA VARIANTS.
RX MEDLINE; 96377761.
RA Dracopoli N.C., Fountain J.W.;
RT "CDKN2A mutations in melanoma.";
RL Cancer Surv. 26:115-132(1996).
RN [6]
RP REVIEW ON VARIANTS.
RX MEDLINE; 96303699.
RA Smith-Soerensen B., Hovig E.;
RT "CDKN2A (p16INK4A) somatic and germline mutations.";
RL Hum. Mutat. 7:294-303(1996).
RN [7]
RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
RX MEDLINE; 94338359.
RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41
RT (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small
RT cell lung carcinomas.";
RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
RN [8]
RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.
RX MEDLINE; 95078916.
RA Hussussan C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,
RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;
RT "Germline p16 mutations in familial melanoma.";
RL Nat. Genet. 8:15-21(1994).
RN [9]
RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.
RX MEDLINE; 95060835.
RA Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
RA Abraham J.M., Meltzer S.J.;
RT "The MTS1 gene is frequently mutated in primary human esophageal
RT tumors.";
RL Oncogene 9:3737-3741(1994).
RN [10]
RP VARIANTS.
RX MEDLINE; 95188190.
RA Okamoto A., Hussan S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zarwala M.,
RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
RT primary and metastatic lung cancer.";
RL Cancer Res. 55:1448-1451(1995).
RN [11]
RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.
RX MEDLINE; 96121580.
RA Walker G.J., Hussussan C.J., Flores J.F., Glendening J.M.,
RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;
RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma
RT kindreds.";
RN [12]

```

RL Hum. Mol. Genet. 4:1845-1852(1995).
 RN [12]
 RN CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
 RX MEDLINE; 95375774.
 RA Ranade K., Hussussian C.J., Sikorski R.S., Varnus H.E., Beach D.,
 RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,
 RA Dracopoli N.C.;
 RA "Mutations associated with familial melanoma impair p16INK4
 RT function.";
 RT Nat. Genet. 10:114-116(1995).
 RL [13]
 RN VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.
 RX MEDLINE; 96323259.
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
 RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
 RA Isselbacher K.J., Sober A.J., Haber D.A.;
 RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in
 RT familial melanoma: analysis of a clinic-based population.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).
 RL [14]
 RN VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.
 RX MEDLINE; 97472457.
 RA Harland M., Meloni R., Gruls N., Pinney E., Brookes S., Spurr N.K.,
 RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,
 RA Bishop D.T., Bishop J.N.;
 RT "Germline mutations of the CDKN2 gene in UK melanoma families.";
 RL Hum. Mol. Genet. 6:2061-2067(1997).
 RL [15]
 RN VARIANTS FAMILIAL MELANOMA.
 RX MEDLINE; 98087572.
 RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Pallierets B.;
 RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone
 RT families in France.";
 RL Hum. Mol. Genet. 7:209-216(1998).
 RL [16]
 RN VARIANTS PANCREATIC CARCINOMA CYS-146.
 RX MEDLINE; 98087572.
 RA Moskaluk C.A., Hruban R.H., Lieman A., Smyrk T., Fusaro L.,
 RA Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;
 RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple
 RT pancreatic carcinomas.";
 RL Hum. Mutat. 12:70-70(1998).
 RL [18]
 RN VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.
 RA Gretsardottir S., Olafsdottir G.H., Borg A.;
 RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,
 RT glioma and carcinoma of the pancreas.";
 RL Hum. Mutat. 12:212-212(1998).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
 CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
 CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
 CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
 CC WIDE RANGE OF TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
 CC INHIBITORS.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
 CC
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 CC
 DR EMBL; L27211; AAA92554.1; -;
 DR EMBL; U12820; AAB60645.1; -;

DR EMBL; U12818; AAB60645.1; JOINED.
 DR EMBL; U12819; AAB60645.1; JOINED.
 DR EMBL; S69804; AAD14048.1; -;
 DR EMBL; X94154; CAA63870.1; -;
 DR PDB; 1BI7; 16-FEB-99.
 DR MIM; 600160; -;
 DR PFAM; PF00023; ank; 3.
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;
 KW Polymorphism; 3D-structure.
 FT DOMAIN 12 141
 FT REPEAT 12 43
 FT REPEAT 44 75
 FT REPEAT 77 109
 FT REPEAT 110 141
 FT VARIANT 14 14
 FT VARIANT 16 16
 FT VARIANT 20 20
 FT VARIANT 20 20
 FT VARIANT 23 23
 FT VARIANT 24 24
 FT VARIANT 24 24
 FT VARIANT 26 26
 FT VARIANT 32 32
 FT VARIANT 33 33
 ... Note: remainder of annotations omitted.
 Query Match 70.8%; Score 692; DB 1; Length 156;
 Best Local Similarity 85.8%; Pred. No. 1.62e-126;
 Matches 103; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
 Db 16 LATAARGRVREVRALLEAGALPNAPNSYGRPRPQVMMGSAARVAELLLHGAEPNCADP 75
 Oy 18 LATPA-RGLVEKVRHSWEAGADPNVGRRAIQVMMGSAARVAELLLHGAEPNCADP 76
 Db 76 ATLTPRVHDAAREGFLDTLVVLHVRAGARLDVDRAGRLPVDLAELGHRDVARVYLRAGA 135
 Oy 77 ATLTPRVHDAAREGFLDTLVVLHVRAGARLDVDRAGRLPVDLAELGHRDVARVYLRAGA 136
 RESULT 5
 ID CDN2_MOUSE STANDARD; PRT; 167 AA.
 AC P51480;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A).
 GN CDKN2A OR P16INK4A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 95380169.
 RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
 RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
 RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
 RL Oncogene 11:635-645(1995).
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
 CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE
 CC PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.

CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES
CC CONTAINED CDK6.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC
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CC
CC EMBL: L76150; AAA85453.1; -
CC MGD: MGI:104738; CDKN2A.
CC DR PFAM: PF00023; ank; 2.
CC KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CC FT DOMAIN 4 152 4 X ANK MOTIF REPEATS.
CC FT REPEAT 4 34 ANK MOTIF 1 (INCOMPLETE).
CC FT REPEAT 35 66 ANK MOTIF 2.
CC FT REPEAT 68 100 ANK MOTIF 3.
CC FT REPEAT 101 152 ANK MOTIF 4.
CC FT VARSPLIC 1 42 MISSING (IN SHORT ISOFORM).
CC SQ SEQUENCE 167 AA; 17870 MW; 88C4588A105ECB8F CRC64;

Query Match 59.5%; Score 581; DB 1; Length 167;
Best Local Similarity 65.6%; Pred. No. 2,75e-101;
Matches 80; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

Db 3 SAADRLARAAGRVHDVRLALLEGVSPNAPNSFGRTPIQVMMGNVHVAALLNLTGADSN 62
QY 13 GSDEGLATPARGLVKVRHSWEAGADPNVNRFGRRATQVMMGSGARVAELLHLHGAEPN 72

Db 63 CEDTTFSPRPVDAAREGFLDTLVVHSGARLDVRDANGRLPDLAERGHQDIVRLR 122
QY 73 CADPATLTPRPVDAAREGFLDTLVVHHRAGARLDVRDANGRLPVDLAERGRDVGAYLR 132

Db 123 SA 124
QY 133 TA 134

RESULT 6
ID CDN2_MONDO STANDARD; PRT; 171 AA.
AC 077617;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)
DE (TUMOR SUPPRESSOR CDKN2A).
GN CDKN2A.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
RN [1]
RP SEQUENCE FROM N.A.
RA Sherburn T.E., Gale J.M., Ley R.D.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC
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CC
CC EMBL: AF064808; AAC23669.1; -
CC DR EMBL: AF064808; AAC23670.1; -
CC DR PFAM: PF00023; ank; 3.
CC KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CC FT DOMAIN 46 169 4 X ANK MOTIF REPEATS.
CC FT REPEAT 46 77 ANK MOTIF 1 (INCOMPLETE).
CC FT REPEAT 78 109 ANK MOTIF 2.
CC FT REPEAT 111 143 ANK MOTIF 3.
CC FT REPEAT 144 169 ANK MOTIF 4.
CC FT VARSPLIC 1 34 MISSING (IN SHORT ISOFORM).
CC SQ SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;

Query Match 58.5%; Score 572; DB 1; Length 171;
Best Local Similarity 69.2%; Pred. No. 2.96e-99;
Matches 83; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

Db 46 SGEKLTEAARGTEVTVTELELTGTPNAVNRFGRSATQVMMGNVRLAAILQYGAPN 105
QY 14 SDEGLA-TPARGLVKVRHSWEAGADPNVNRFGRRATQVMMGSGARVAELLHLHGAEPN 72

Db 106 TPDPTTLTPVHDAAREGFLDTLMLHHRAGARLDVRDANGRLPVDLAEEQGHLLVAYLR 165
QY 73 CADPATLTPRPVDAAREGFLDTLVVHHRAGARLDVRDANGRLPVDLAERGRDVGAYLR 132

RESULT 7
ID CDN7_HUMAN STANDARD; PRT; 166 AA.
AC P55273; Q13102;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
GN CDKN2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RX MEDLINE: 96121373.
RA Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J.,
RA Lahti J.M., Sherr C.J., Downing J.R.;
RT "Molecular cloning, expression pattern, and chromosomal localization
RT of human CDKN2D/INK4d, an inhibitor of cyclin D-dependent kinases.";
RL Genomics 29:623-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96362662.
RA Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,
RA Zariwala M., Matera A.G., Xiong Y.;
RT "Isolation and characterization of p19INK4d, a p16-related inhibitor
RT specific to CDK6 and CDK4.";
RL Mol. Biol. Cell 7:57-70(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-THYMUS;
RX MEDLINE: 95237949.
RA Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;
RT "Identification of human and mouse p19, a novel CDK4 and CDK6
RT inhibitor with homology to p16ink4.";
RL Mol. Cell. Biol. 15:2682-2688(1995).
RN [4]
RP SEQUENCE FROM N.A.
RA Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
RA Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
RA Bishop D.T.;
RT "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.";

Db 66 KDTGFA-VIHDARAGFLDTVQALLERQADVNTEDNEGNLPLHLAAKEGHLPVVEFLMK 124
| : : : : | | | | | : : : : | | | | : |
Qy 74 ADPATLTPRVDAAREGEFLDTLVVHLHRAGRLDVRDANGRLPVDLAERGRHVDVAGYLRT 133
| : : : : | | | | | : : : : | | | | : |
Db 125 HTA 127
| : : : : | | | | | : : : : | | | | : |
Qy 134 ATG 136
| : : : : | | | | | : : : : | | | | : |
RESULT 11
ID DAPK_HUMAN STANDARD; PRT; 1431 AA.
AC P53355;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
GN DAPK1 OR DAPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95129831.
RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT "Identification of a novel serine/threonine kinase and a novel 15-kD
protein as potential mediators of the gamma interferon-induced cell
death.";
RL Genes Dev. 9:15-30(1995).
RN [2]
RP REVISIONS TO 164-171.
RA Feinstein E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
DEATH.
CC -1- PTM: AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 8 ANK REPEATS.

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DR EMBL; X76104; CAA53712.1; -;
DR HSP; Q63450; 1A06.
DR MIM; 600831; -;
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PFAM; PF00023; ank; 8.
DR PFAM; PF00069; Pkinase; 1.
DR PFAM; PF00531; Death; 1.
KW Phosphatase; Serine/threonine-protein kinase; Calmodulin-binding;
KW phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
FT DOMAIN 13 266 PROTEIN KINASE
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT DOMAIN 267 334 CALMODULIN-BINDING.
FT DOMAIN 373 637 8 X ANK MOTIF REPEATS.
FT REPEAT 373 405 ANK MOTIF 1.
FT REPEAT 406 438 ANK MOTIF 2.
FT REPEAT 439 471 ANK MOTIF 3.
FT REPEAT 473 505 ANK MOTIF 4.
FT REPEAT 506 538 ANK MOTIF 5.
FT REPEAT 539 571 ANK MOTIF 6.
FT REPEAT 572 604 ANK MOTIF 7.
FT REPEAT 605 637 ANK MOTIF 8.

FT DOMAIN 1313 1397 DEATH DOMAIN.
FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
SQ SEQUENCE 1431 AA; 160017 MW; 9EB84811004A155B CRC64;
Query Match 14.3%; Score 140; DB 1; Length 1431;
Best Local Similarity 32.2%; Pred. No. 2.39e-08;
Matches 37; Conservative 23; Mismatches 53; Indels 2; Gaps 2;
Db 517 LTASARGYHDIVCELAEGHAGDLNACDKGHLALHAYRRCOMVEIKTLISQCGFVDYQDR 576
| : : : : | | | | | : : : : | | | | : |
Qy 18 LATPARGLVKVRHSWEAGADPNVNGVRRRAIQVMMGMSAR-VAELLHLHGAEPCADP 76
| : : : : | | | | | : : : : | | | | : |
Db 577 HGNT-PLHVACKDGNFIVVALCEANCLNLSNKYGRTPHLAANNGLDVRVL 630
| : : : : | | | | | : : : : | | | | : |
Qy 77 ATLTPRVDAAREGEFLDTLVVHLHRAGRLDVRDANGRLPVDLAERGRHVDVAGYL 131
| : : : : | | | | | : : : : | | | | : |
RESULT 12
ID ANK1_HUMAN STANDARD; PRT; 1880 AA.
AC P16157;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).
GN ANK1 OR ANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A. PARTIAL SEQUENCE, AND VARIANTS.
RX TISSUE-HEMATOPOIETIC;
RX MEDLINE; 90158830.
RA Lux S.E., John K.M., Bennett V.;
RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT structure with homology to tissue-differentiation and cell-cycle
RT control proteins.";
RL Nature 344:36-42(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90175370.
RA Lambert S.C., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,
RA Cheung M.C., Kan Y.W., Palek J.;
RT "cDNA sequence for human erythrocyte ankyrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
RN [3]
RP VARIANT HS ILE-462.
RX MEDLINE; 96225450.
RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
RT "Ankyrin-1 mutations are a major cause of dominant and recessive
RT hereditary spherocytosis.";
RL Nat. Genet. 13:214-218(1996).
CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
CC NA-K ATPASE, TO THE LIMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTE ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
CC PLASMA MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY
CC ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
CC VARIANT 2.1.
CC -1- PTM: REGULATED BY PHOSPHORYLATION.
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
CC -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE
CC HEREDITARY SPHEROCYTOSIS (HS).
CC -1- SIMILARITY: CONTAINS 24 ANK REPEATS.

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FT DISULFID 106 BY SIMILARITY.
FT DISULFID 111 BY SIMILARITY.
FT DISULFID 130 BY SIMILARITY.
FT DISULFID 139 BY SIMILARITY.
FT DISULFID 145 BY SIMILARITY.
FT DISULFID 150 BY SIMILARITY.
FT DISULFID 167 BY SIMILARITY.
FT DISULFID 183 BY SIMILARITY.
FT DISULFID 188 BY SIMILARITY.
FT DISULFID 205 BY SIMILARITY.
FT DISULFID 221 BY SIMILARITY.
FT DISULFID 226 BY SIMILARITY.
FT DISULFID 244 BY SIMILARITY.
FT DISULFID 260 BY SIMILARITY.
FT DISULFID 265 BY SIMILARITY.
FT DISULFID 282 BY SIMILARITY.
FT DISULFID 298 BY SIMILARITY.
FT DISULFID 305 BY SIMILARITY.
FT DISULFID 322 BY SIMILARITY.
FT DISULFID 338 BY SIMILARITY.
FT DISULFID 343 BY SIMILARITY.
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FT DISULFID 380 BY SIMILARITY.
FT DISULFID 399 BY SIMILARITY.
FT DISULFID 415 BY SIMILARITY.
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FT DISULFID 439 BY SIMILARITY.
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FT DISULFID 498 BY SIMILARITY.
FT DISULFID 515 BY SIMILARITY.
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FT DISULFID 536 BY SIMILARITY.
FT DISULFID 553 BY SIMILARITY.
FT DISULFID 569 BY SIMILARITY.
FT DISULFID 574 BY SIMILARITY.
FT DISULFID 590 BY SIMILARITY.
FT DISULFID 606 BY SIMILARITY.
FT DISULFID 611 BY SIMILARITY.
FT DISULFID 628 BY SIMILARITY.
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FT DISULFID 665 BY SIMILARITY.
FT DISULFID 681 BY SIMILARITY.
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FT DISULFID 703 BY SIMILARITY.
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FT DISULFID 740 BY SIMILARITY.
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FT DISULFID 799 BY SIMILARITY.
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FT DISULFID 832 BY SIMILARITY.
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FT DISULFID 877 BY SIMILARITY.
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FT DISULFID 910 BY SIMILARITY.
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FT DISULFID 1008 BY SIMILARITY.
FT DISULFID 1024 BY SIMILARITY.
FT DISULFID 1029 BY SIMILARITY.
FT DISULFID 1046 BY SIMILARITY.

FT DISULFID 1062 BY SIMILARITY.
FT DISULFID 1067 BY SIMILARITY.
FT DISULFID 1082 BY SIMILARITY.
FT DISULFID 1093 BY SIMILARITY.
FT DISULFID 1100 BY SIMILARITY.
FT DISULFID 1121 BY SIMILARITY.
FT DISULFID 1130 BY SIMILARITY.
FT DISULFID 1141 BY SIMILARITY.
FT DISULFID 1159 BY SIMILARITY.
FT DISULFID 1168 BY SIMILARITY.
FT DISULFID 1183 BY SIMILARITY.
FT DISULFID 1170 BY SIMILARITY.
FT DISULFID 1197 BY SIMILARITY.
FT DISULFID 1206 BY SIMILARITY.
FT DISULFID 1217 BY SIMILARITY.
FT DISULFID 1224 BY SIMILARITY.
FT DISULFID 1237 BY SIMILARITY.
FT DISULFID 1252 BY SIMILARITY.
FT DISULFID 1263 BY SIMILARITY.
FT DISULFID 1270 BY SIMILARITY.
FT DISULFID 1283 BY SIMILARITY.
FT DISULFID 1292 BY SIMILARITY.
FT DISULFID 1294 BY SIMILARITY.
FT DISULFID 1310 BY SIMILARITY.
FT DISULFID 1321 BY SIMILARITY.
FT DISULFID 1335 BY SIMILARITY.
FT DISULFID 1344 BY SIMILARITY.
FT DISULFID 1351 BY SIMILARITY.
FT DISULFID 1362 BY SIMILARITY.
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FT DISULFID 1382 BY SIMILARITY.
FT DISULFID 1390 BY SIMILARITY.
FT DISULFID 1401 BY SIMILARITY.
FT DISULFID 1412 BY SIMILARITY.
FT DISULFID 1414 BY SIMILARITY.
FT DISULFID 1423 BY SIMILARITY.

...
Note: remainder of annotations omitted.

Query Match 13.6%; Score 133; DB 1; Length 2524;
Best Local Similarity 33.6%; Pred. No. 3.72e-07;
Matches 38; Conservative 27; Mismatches 43; Indels 5; Gaps 5;

Db 1996 LILARLAVEGVEELINAHADVNAVDFGKSALHWAANVNDAAVLLKNSANKD-MQ 2054

QY 18 LATPARGLVE-KVHSWEAGADPNVRFGRATQ-VMMGSGARVAEILLHGHAEPCAD 75

Db 2055 NKKEETSLFLAAREGSYETAKVLLDHYANR-DITDHMDRLPRDIAOERMHDI 2106

QY 76 PATLTRPVHDAAREGFLDTL-VLHHRAGARLDVRDAGRLPVDLAERGRHDV 127

RESULT 15
ID ANKC_HUMAN STANDARD; PRT; 1839 AA.
AC Q01485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)
DE (FRAGMENT).
GN ANK2.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN STEM;
RX MEDLINE; 91302466.
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).

RN [2]
RP SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE; 92009921.
RA Tse W.T., Menninger J.C., Yang-Peng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN

(TM)

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	598	61.2	86	Q9X552	P15/WTCL2/CDKN2B (FRAGM	3.48e-103
2	585	60.0	115	Q16361	CELL CYCLE NEGATIVE RE	1.61e-99
3	582	59.6	102	Q9X551	P16/CDKN2A/MTS1 (FRAGM	1.24e-98
4	574	58.8	108	P97310	CYCLIN DEPENDENT KINAS	7.33e-98
5	570	58.3	168	Q11088	CYCLIN DEPENDENT KINAS	5.65e-97
6	563	57.6	86	Q9Z1C1	CYCLIN-DEPENDENT KINAS	2.00e-95
7	551	56.4	86	Q54846	CYCLIN-DEPENDENT KINAS	8.99e-93
8	479	49.0	113	Q9Z1C2	CYCLIN-DEPENDENT KINAS	5.81e-77
9	364	37.3	124	P70067	CDKN2X PROTEIN.	3.66e-52
10	358	36.6	58	Q97886	CYCLIN-DEPENDENT KINAS	6.26e-51
11	357	36.5	124	Q9W618	P13CDKN2X.	1.02e-50
12	309	31.6	78	Q15125	ALTERNATIVE SPLICED FO	1.14e-40
13	186	19.0	44	Q9Z1C0	CYCLIN-DEPENDENT KINAS	3.15e-16
14	141	14.4	745	Q91344	D20208.1 (NOVEL RAT E	5.76e-08
15	140	14.3	1719	Q13768	ALT. ANKYRIN (VARIANT	5.57e-08
16	140	14.3	1856	Q99407	ANKYRIN.	5.57e-08
17	139	14.2	800	Q43988	HOMEBOX-CONTAINING PR	8.24e-08
18	139	14.2	837	Q63618	ESPIN	8.24e-08
19	137	14.0	1098	Q61304	ANKYRIN 1, ERYTHROID (1.80e-07
20	137	14.0	1848	Q61302	ANKYRIN 1, ERYTHROID (1.80e-07

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H.,
 RA PARRY D., PETERS G., KAMB A.;
 RA "Complex structure and regulation of the P16 (MTS1) locus";
 RT Cancer Res. 55:2988-2994(1995).
 DR EMBL; S78535; AAC60650.1; -;
 DR HSSP; P42771; 1BI7.
 FT NON_TER 1
 SQ SEQUENCE 115 AA; 12334 MW; F5BF54B CRC32;
 Query Match 60.0%; Score 586; DB 6; Length 115;
 Best Local Similarity 95.3%; Pred. No. 1.61e-100;
 Matches 82; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Db 9 QVMMGSAVVAELLHGAEPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVRDA 68
 Qy 51 QVMMGSAVVAELLHGAEPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVRDA 110
 Db 69 WGRLPVDAEERGHDRVARYLRAAG 94
 Qy 111 WGRLPVDAEERGHDRVAGYLRTATG 136
 RESULT 3
 ID Q9XS51 PRELIMINARY; PRT; 102 AA.
 AC Q9XS51;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE P16(CDKN2A/MTS1 (FRAGMENT)).
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PBMC;
 RA OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
 RA NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
 RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
 RT and p15(MTS2/CDKN2B)";
 RL submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB010807; BAA33540.1; -;
 FT NON_TER 1
 FT NON_TER 102
 SQ SEQUENCE 102 AA; 10824 MW; 8C3094E9 CRC32;
 Query Match 59.6%; Score 582; DB 6; Length 102;
 Best Local Similarity 92.9%; Pred. No. 1.24e-99;
 Matches 79; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 1 VMMGSAVVAELLHGAEPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVRDAW 60
 Qy 52 VMMGSAVVAELLHGAEPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVRDAW 111
 Db 61 GRPLPVDLAERGHDRVYLRARTG 85
 Qy 112 GRPLPVDLAERGHDRVAGYLRTATG 136
 RESULT 4
 ID P97510 PRELIMINARY; PRT; 168 AA.
 AC P97510; P97937;
 DT 01-MAY-1999 (Tremblrel. 03, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR
 DE PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16, INHIBITS CDK4)
 DE (P16INK4A) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
 GN CDKN2A OR E1ALPHA OR P16INK4A OR CDKN2A.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DBA/2N; TISSUE-SPLEEN;
 RX MEDLINE; 98151529.
 RA ZHANG S., RAMSAY E.S., MOCK B.A.;
 RT "cdk2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
 RT p19ARF, is a candidate for the plasmacytoma susceptibility locus,
 RT Pctrl";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
 RN [2]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN-VARIOUS STRAINS;
 RX MEDLINE; 97179476.
 RA HERZOG C.R., YOU M.;
 RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
 RT suppressor gene";
 RL Mamm. Genome 8:65-66(1997).
 RN [3]
 RP SEQUENCE OF 1-155 FROM N.A.
 RC STRAIN-C57BL/6J X DBA;
 RA MALUMBRES M., DE CASTRO I., SANTOS J., MELENDEZ B., MANGUES R.,
 RA SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.;
 RL submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN-DBA/2 AND C57BL/6;
 RX MEDLINE; 95380169.
 RA QUELLE D.E., ASHMUN R.A., HANNON G.J., REHBERGER P.A., TRONO D.,
 RA RICHTER K.H., WALKER C., BEACH D., SHERR C.J., SERRANO M.;
 RT "Cloning and characterization of murine p16INK4a and p15INK4b genes";
 RL Oncogene 11:635-645(1995).
 RN [5]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN-DBA/2 AND C57BL/6;
 RA GRESSANI K.M., ROLLINS L.A., MILLER M.S.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 1-11 FROM N.A.
 RC STRAIN-ICR SWISS;
 RX MEDLINE; 97128829.
 RA SOLOFF E.V., HERZOG C.R., YOU M.;
 RT "The 5'-flanking region of the E1 alpha form of the murine p16INK4a
 RT (MTS1) gene";
 RL Gene 180:213-215(1996).
 RN [7]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN-CAST/EI, C57BL/6J AND RF/J, MOLE/EI AND MUS MUSCULUS;
 RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
 RA PELLICER A., FERNANDEZ-PIQUERAS J.;
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
 RT in mouse inbred strains";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF044336; AAC08963.1; -;
 DR EMBL; U49280; AAC00052.1; -;
 DR EMBL; U66087; AAB39600.1; -;
 DR EMBL; U66086; AAB39600.1; JOINED.
 DR EMBL; AF004588; AAB61416.1; -;
 DR EMBL; U47018; AAC52987.1; -;
 DR EMBL; U79628; AAD00226.1; -;
 DR EMBL; U79625; AAD00223.1; -;
 DR EMBL; U79627; AAD00225.1; -;
 DR HSSP; P42771; 1BI7.
 DR MGD; MGI-104738; Cdkn2a.
 DR PFAM; PF00023; ank; 3.
 KW Kinase; Cyclin.
 SQ SEQUENCE 168 AA; 17941 MW; 89AD5E62 CRC32;
 Query Match 58.8%; Score 574; DB 11; Length 168;
 Best Local Similarity 65.0%; Pred. No. 7.35e-98;
 Matches 80; Conservative 21; Mismatches 21; Indels 1; Gaps 1;

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Db 3 SAADRLARAAQGRVHDVRLLEAGVSPNAPNSFGRTPIQVMGMGNVHVAALLNNGADS 62
QY 13 GSDEGLA-TPARGLVKVRHWSWEAGADPNVNGRRAIQVMGMSARVAELLHLHGAEP 71
Db 63 NCDPTTFSRPHVDAAREGFDLTIVLHSGARLDVDAWGRPLDIAQERGHODIVRYL 122
QY 72 NCADPATLTRPVHDAAREGFDLTIVLHSGARLDVDAWGRPLDIAQERGHODIVRYL 131
Db 123 RSA 125
QY 132 RTA 134

RESULT 5
ID 089088 PRELIMINARY; PRT; 168 AA.
AC 089088;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
GN CDKN2A OR E1AHPA OR p16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CANP; TISSUE-SPLEEN;
RX MEDLINE; 98151529.
RA ZHANG S., RAMSAY E.S., MOCK B.A.;
RT "cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
RT p19ARF, is a candidate for the plasmacytoma susceptibility locus,
RT Petri.";
RL Mamm. Genome 8:65-66(1997).
RN [2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-MA/M4J;
RX MEDLINE; 97179476.
RA HERZOG C.R., YOU M.;
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
RT suppressor gene.";
RL Mamm. Genome 8:65-66(1997).
RN [3]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA PELLICER A., FERNANDEZ-PIQUERAS J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044335; AAC08962.1; -
DR EMBL; U49279; AAC00051.1; -
DR EMBL; U79626; RAD00224.1; -
DR HSP; P42771; 1B17.
DR PFAM; PF00023; ank. 3.
KW Kinase; Cyclin.
SQ SEQUENCE 168 AA; 17915 MW; F0087F4C CRC32;

Query Match 58.3%; Score 570; DB 11; Length 168;
Best Local Similarity 64.2%; Pred. No. 5.65e-97;
Matches 79; Conservative 22; Mismatches 21; Indels 1; Gaps 1;

Db 3 SAADRLARAAQGRVHDVRLLEAGVSPNAPNSFGRTPIQVMGMGNVHVAALLNNGADS 62
QY 13 GSDEGLA-TPARGLVKVRHWSWEAGADPNVNGRRAIQVMGMSARVAELLHLHGAEP 71
Db 63 NCDPTTFSRPHVDAAREGFDLTIVLHSGARLDVDAWGRPLDIAQERGHODIVRYL 122
QY 72 NCADPATLTRPVHDAAREGFDLTIVLHSGARLDVDAWGRPLDIAQERGHODIVRYL 131
Db 123 RSA 125
QY 132 RTA 134

RESULT 7
ID 054846 PRELIMINARY; PRT; 86 AA.
AC 054846;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J;
RA MALUMBRES M., PELLICER A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015460; AAB94534.1; -
DR HSP; P42771; 1B17.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 86 AA; 9237 MW; FEC97F63 CRC32;

Query Match 56.4%; Score 551; DB 11; Length 86;
Best Local Similarity 89.5%; Pred. No. 8.99e-93;
Matches 77; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 VMMGSAQVAELLHLHGAEPNCADPATLTRPVHDAAREGFDLTIVLHSGARLDVDAW 60
QY 52 VMMGSAQVAELLHLHGAEPNCADPATLTRPVHDAAREGFDLTIVLHSGARLDVDAW 111
Db 61 GRPVDLAEERGHODIARYLHAATGD 86
QY 112 GRPVDLAEERGHODIARYLHAATGD 137

Query Match 57.6%; Score 563; DB 11; Length 86;
Best Local Similarity 91.9%; Pred. No. 2.00e-95;
Matches 79; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 1 VMMGSAQVAELLHLHGAEPNCADPATLTRPVHDAAREGFDLTIVLHSGARLDVDAW 60
QY 52 VMMGSAQVAELLHLHGAEPNCADPATLTRPVHDAAREGFDLTIVLHSGARLDVDAW 111
Db 61 GRPVDLAEERGHODIARYLHAATGD 86
QY 112 GRPVDLAEERGHODIARYLHAATGD 137

RESULT 7
ID 054846 PRELIMINARY; PRT; 86 AA.
AC 054846;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J;
RA MALUMBRES M., PELLICER A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015460; AAB94534.1; -
DR HSP; P42771; 1B17.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 86 AA; 9237 MW; FEC97F63 CRC32;

Query Match 56.4%; Score 551; DB 11; Length 86;
Best Local Similarity 89.5%; Pred. No. 8.99e-93;
Matches 77; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 VMMGSAQVAELLHLHGAEPNCADPATLTRPVHDAAREGFDLTIVLHSGARLDVDAW 60
QY 52 VMMGSAQVAELLHLHGAEPNCADPATLTRPVHDAAREGFDLTIVLHSGARLDVDAW 111
Db 61 GRPVDLAEERGHODIARYLHAATGD 86
QY 112 GRPVDLAEERGHODIARYLHAATGD 137

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QY	35	AGADPNVNGRRRAIQVMMGSGARVAELLLUHGAPNCADPATLTRVPHDAREGFL	92
RESULT	11		
ID	Q9W6I8	PRELIMINARY; PRT; 124 AA.	
AC	Q9W6I8;		
DT	01-NOV-1999	(TREMBLrel. 12, Created)	
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)	
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)	
DE	P13CDKN2X.		
DE	CDKN2X.		
GN	Xiphophorus helleri.		
OS	Xiphophorus helleri.		
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorphia;		
OC	Cyprinodontiformes; Cyprinodontoidae; Poeciliidae; Xiphophorus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-RIO SARABIA;		
RC	KAZIANIS S., MORIZOT D.C., DELLA COLETTA L., JOHNSTON D.A.,		
RA	WOOLCOCK B., VIELKIND J.R., NAYEN R.S.;		
RT	"Comparative Structure and Characterization of a CDKN2 Gene in a		
RT	Xiphophorus Fish Melanoma Model.;"		
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF132500; AAD21313.1; -.		
SQ	SEQUENCE 124 AA; 13049 MW; DA386E94 CRC32;		
Query Match	35.58; Score 357; DB 13; Length 124;		
Best Local Similarity	52.58; Pred. No. 1.02e-50;		
Matches	63; Conservative 18; Mismatches 38; Indels 1; Gaps		
DB	4	EDELTTAAKGTAEVALLLOGAPVNGVNSGRRRAIQVMMGSGSEVARLLITRGADPNV	63

QY 15 DEGLATPA-RGLVKRHSWEAGADPNGVNRFRRAIQVMGMSARVAELLLHGAEPNC 73
 Db 64 TDKSTGATPLHDAARTGFLDTVQLLEAGADPQARDKNCPLFDILARONGHTDVAVLET 123
 QY 74 ADPATLTRPVHDAAREGFLDTLVHLHRAGARLDVRDANGRLPVDLAERGHDRVAGYLRT 133

RESULT 12
 ID O15125 PRELIMINARY; PRT; 78 AA.
 AC O15125;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE ALTERNATIVE SPLICED FORM OF P15 CDK INHIBITOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97373727.
 RA TSUBARI M., TIHONEN E., LAIHO M.;
 RT "Cloning and characterization of p10, an alternatively spliced form of
 RT p15 cyclin-dependent kinase inhibitor.";
 RL Cancer Res. 57:2966-2973(1997).
 DR EMBL; AF004819; AAB69989.1; -.
 DR HSSP; P42773; 1B09.
 SQ SEQUENCE 78 AA; 8078 MW; 706939FA CRC32;

Query Match 31.6%; Score 309; DB 4; Length 78;
 Best Local Similarity 88.7%; Pred. No. 1.14e-40;
 Matches 47; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
 Db 1 MREENKMPGSGGSDGLASAAAGLVKRYQLLEAGADPNGVNRFRRAIQV 53
 QY 1 MREENKMPGSGGSDGLATPA-RGLVKRHSWEAGADPNGVNRFRRAIQV 52

RESULT 13
 ID Q921C0 PRELIMINARY; PRT; 44 AA.
 AC Q921C0;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
 GN INK4B.
 OS Mus spretus (Western wild mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRET/BI;
 RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MARTIN-RIVERA L.,
 RA MALUMBRES M., SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.,
 RT "Comparative analysis of the p16 (INK4a) and p15 (INK4b) DNA sequences
 RT in mouse inbred strains.";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U80416; AAD00359.1; -.
 DR HSSP; P42773; 1IHB.
 KW Kinase; Cyclin.
 FT NON_TER 44
 SQ SEQUENCE 44 AA; 4537 MW; 21E5F311 CRC32;

Query Match 19.0%; Score 186; DB 11; Length 44;
 Best Local Similarity 71.4%; Pred. No. 3.15e-16;
 Matches 30; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
 Db 3 GGSSDAGLATAAARGOVETVROLLEAGADPNALNFRGRRIQ 44
 QY 11 GGSDEGLATPA-RGLVKRHSWEAGADPNGVNRFRRAIQ 51

RESULT 14
 ID Q921C0 PRELIMINARY; PRT; 44 AA.
 AC Q921C0;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
 GN INK4B.
 OS Mus spretus (Western wild mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRET/BI;
 RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MARTIN-RIVERA L.,
 RA MALUMBRES M., SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.,
 RT "Comparative analysis of the p16 (INK4a) and p15 (INK4b) DNA sequences
 RT in mouse inbred strains.";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U80416; AAD00359.1; -.
 DR HSSP; P42773; 1IHB.
 KW Kinase; Cyclin.
 FT NON_TER 44
 SQ SEQUENCE 44 AA; 4537 MW; 21E5F311 CRC32;

Query Match 19.0%; Score 186; DB 11; Length 44;
 Best Local Similarity 71.4%; Pred. No. 3.15e-16;
 Matches 30; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
 Db 3 GGSSDAGLATAAARGOVETVROLLEAGADPNALNFRGRRIQ 44
 QY 11 GGSDEGLATPA-RGLVKRHSWEAGADPNGVNRFRRAIQ 51

ID Q9Y544 PRELIMINARY; PRT; 745 AA.
 AC Q9Y544;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE DJ20208.1 (NOVEL RAT ESPIN LIKE PROTEIN CONTAINING ANK REPEATS)
 DE (FRAGMENT).
 GN DJ20208.1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOWDEN P.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031848; CAB46197.1; -.
 FT NON_TER 745
 SQ SEQUENCE 745 AA; 78960 MW; F1AB0F4C CRC32;

Query Match 14.4%; Score 141; DB 4; Length 745;
 Best Local Similarity 44.9%; Pred. No. 3.76e-08;
 Matches 35; Conservative 12; Mismatches 29; Indels 2; Gaps 2;
 Db 251 GHTKVLWSLLHGGEIS-ADLWGGT-PLHDAENGELECCOILVVGAEVDVDRDGYTA 308
 QY 56 GSARVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLVHLHRAGARLDVRDANGRLP 115
 Db 309 ADLSDFNGHSHCTRYLRT 326
 QY 116 VDLAERGHDRVAGYLRT 133

RESULT 15
 ID Q13768 PRELIMINARY; PRT; 1719 AA.
 AC Q13768;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE ALT. ANKYRIN (VARIANT 2.2).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HEMATOPOIETIC;
 RX MEDLINE; 90158830.
 RA LUX S.E., JOHN K.M., BENNETT V.;
 RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
 RT structure with homology to tissue-differentiation and cell-cycle
 RT control proteins.";
 RL Nature 344:36-42(1990).
 DR EMBL; X16609; CAA34611.1; -.
 DR HSSP; P00421; 1AWC.
 DR PFAM; PF00023; ank; 22.
 DR PFAM; PF00531; death; 1.
 DR PFAM; PF00791; 205; 1.
 SQ SEQUENCE 1719 AA; 189010 MW; CE3D699D CRC32;

Query Match 14.3%; Score 140; DB 4; Length 1719;
 Best Local Similarity 32.3%; Pred. No. 5.57e-08;
 Matches 42; Conservative 25; Mismatches 55; Indels 8; Gaps 8;
 Db 493 NANPNLATTAG-HTPLHIAAREGHVETVLLLEKEASOACMTKKGFTPLHVAARYGKVRV 551
 QY 3 EENKMPGSGGSDGLATPA-RGLVKRHSWEAGADPNGVNRFRRAIQVMM-GSARV 60
 Db 552 AELLERDAHNAACKNGLT-PLHVAHVHNNLDIVKLLPRGGSP-HSP-ANNGYTPPLHI 608
 QY 61 AELLHGAEPNCADPATLTRPVHDAAREGFLDTLVHLHRAGARLDVRDANGRLPVDL 118
 Db 609 AAKONOVEVA 618
 QY 119 AEERGHDRVA 128

Search completed: Thu Jul 20 08:39:54 2000
Job time : 21 secs.
